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"Examiner Search Notes"

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James Martinell
Primary Examiner 1631

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 01:43:47 ; Search time 210.069 Seconds
(without alignments)
8342.279 Million cell updates/sec

Title: US-09-938-842a-1034
Perfect score: 1071
Sequence: 1 atggcgacacatcagacagct.....cagcgatcagacacatga 1071

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

1 number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/1/ina/6CTUS_COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfillseq1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	4.1	7218	1	US-08-232-463-14
2	41	3.8	7218	1	US-08-232-463-14
3	40.4	3.8	915	4	US-09-248-796A-6057
4	34	3.2	654	4	US-08-956-171E-613
5	34	3.2	654	4	US-08-781-986A-613
6	33.4	3.1	601	4	US-09-949-016-33921
7	33.4	3.1	601	4	US-09-949-016-133049
8	33.4	3.1	34068	4	US-09-949-016-15489
9	33.4	3.1	51711	4	US-09-949-016-12589
10	33	3.1	2127	4	US-09-252-991A-8192
11	33	3.1	2874	4	US-09-252-991A-8112
12	32.8	3.1	4403765	3	US-09-103-840A-2
13	32.2	3.0	2406	3	US-09-632-098-5
14	32.2	3.0	2406	3	US-10-177-308-5
15	32.2	3.0	2439	3	US-09-632-098-6
16	32.2	3.0	2439	4	US-10-177-308-6
17	31.6	3.0	601	4	US-09-949-016-121693
18	31.6	3.0	601	4	US-09-949-016-121694
19	31.6	3.0	601	4	US-09-949-016-121695
20	31.6	3.0	1104	4	US-09-902-540-6871
21	31.6	3.0	1141	4	US-09-906-708B-22
22	31.6	3.0	4019	4	US-09-902-540-583
23	31.6	3.0	15192	4	US-09-949-016-15143
24	31.4	2.9	4411529	3	US-09-103-840A-1
25	31	2.9	3842	4	US-09-976-594-279
26	30.6	2.9	412	3	US-08-961-083-111
27	30.6	2.9	412	4	US-09-536-784-111

C 28	30.6	2.9	894	4	US-09-540-236-1485	Sequence 1485, Ap
C 29	30.6	2.9	912	4	US-09-489-039A-3905	Sequence 3905, Ap
C 30	30.6	2.9	963	4	US-09-270-767-2582	Sequence 2582, Ap
C 31	30.6	2.9	963	4	US-09-270-767-17864	Sequence 17864, A
C 32	30.6	2.9	1288	4	US-09-620-312D-546	Sequence 546, App
C 33	30.6	2.9	2322	4	US-09-270-767-1512	Sequence 1512, Ap
C 34	30.6	2.9	2322	4	US-09-270-767-16794	Sequence 16794, A
C 35	30.6	2.9	2427	4	US-09-270-767-4937	Sequence 4937, Ap
C 36	30.6	2.9	2427	4	US-09-270-767-20219	Sequence 20219, A
C 37	30.6	2.9	6693	3	US-08-961-527-195	Sequence 195, App
C 38	30.6	2.9	49617	4	US-09-596-002-28	Sequence 28, App
C 39	30.6	2.9	250715	4	US-09-949-016-13294	Sequence 13294, A
C 40	30.4	2.8	2172	1	US-07-982-712-1	Sequence 1, App11
C 41	30.4	2.8	7766	3	US-09-125-619-3	Sequence 3, App11
C 42	30.4	2.8	7766	4	US-10-222-566-3	Sequence 3, App11
C 43	30.4	2.8	7766	4	US-10-143-024A-3	Sequence 3, App11
C 44	30.4	2.8	580073	4	US-08-545-528D-1	Sequence 1, App11
C 45	30.2	2.8	306	4	US-09-513-999C-11186	Sequence 11186, A

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHIEFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29, 768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZpT-F18
; US-08-232-463-14
Query Match 4.1%; Score 44; DB 1; Length 7218;

Db 655 ATATGATGCTGCTTATCTGTGTGTAACCTCTGTCTGATGTTCTCAAGAACTTGG 714
Qy 907 TCGGTATGCGTC 920
Db 715 GCTGCTTGGCTGC 728

RESULT 4

US-08-956-171E-613/C

; Sequence 613, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunesh

; Gail H. Choi

; Patrick S. Dillon

; Craig A. Roosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIORITY INFORMATION:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 613:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 654 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 613:

US-08-956-171E-613

Query Match 3.2%; Score 34; DB 4; Length 654;

Best Local Similarity 48.0%; Pred. No. 1.3;

Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 472 ATGGGGAATCTGATGAAGAAAGTAAAGCACTTTAAAGTGAATATAGAC 531
Db 455 ATTACTGCAATGATGAAGATGAAGATAGATGCGCAAAATATCTGTTAATTGCC 396
Qy 533 ATAAAGCAGCGGTTTCACTTCCTCGGTTTAACTTCAATTCGACGACGACGATC 591
Db 395 TTAGGATAGACTTTTAAAGGATCTGATTCACGACGATTAAGTCTACTTCTGTA 336
Qy 592 CAACCTCCGCAAGCTTGGCATCATCACTGTGGCTCAGCAACTTTCGCGCAAGAAAG 651
Db 335 CCACCAACGAAATCCGCGACTAATATATACGCTTAAGAAACGAGATACCAACCA 276

Qy 652 TATCCGATGCGGCTATTTCAT 673
Db 275 AACGGTGTGCGCTTTGTAT 254

RESULT 5

US-08-781-986A-613/C

; Sequence 613, Application US/08781986A

; Patent No. 6737248

; GENERAL INFORMATION:

; APPLICANT: Charles Kunesh

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIORITY INFORMATION:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: PB248BP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 613:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 654 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-781-986A-613

Query Match 3.2%; Score 34; DB 4; Length 654;

Best Local Similarity 48.0%; Pred. No. 1.3;

Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 472 ATGGGGAATCTGATGAAGAAAGTAAAGCACTTTAAAGTGAATATAGAC 531
Db 455 ATTACTGCAATGATGAAGATGAAGATAGATGCGCAAAATATCTGTTAATTGCC 396
Qy 533 ATAAAGCAGCGGTTTCACTTCCTCGGTTTAACTTCAATTCGACGACGACGATC 591
Db 395 TTAGGATAGACTTTTAAAGGATCTGATTCACGACGATTAAGTCTACTTCTGTA 336
Qy 592 CAACCTCCGCAAGCTTGGCATCATCACTGTGGCTCAGCAACTTTCGCGCAAGAAAG 651
Db 335 CCACCAACGAAATCCGCGACTAATATATACGCTTAAGAAACGAGATACCAACCA 276
Qy 652 TATCCGATGCGGCTATTTCAT 673
Db 275 AACGGTGTGCGCTTTGTAT 254

RESULT 6

US-09-949-016-33921

; Sequence 33921, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33921
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-33921

Query Match
Best Local Similarity 3.1%; Score 33.4; DB 4; Length 601;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGAGGCAAGATCAACTTAAGAGCCGTTGATCTTAACCATCATCAAGCGCTCAGAA 88
DB 100 TTGCTGTCCTTTGGAAAGTCATTTGCACTGATGACACAAAGGCTCATCTCTGAA 159
QY 89 AGCTGCAAACTTCAAGCCTTTCCAGTAATCCCAAGAGAGCTGTGAGCCCAAGCGG 148
DB 160 TCGTCACTCTGCAGAAAGCAGAAAGGCGCATTCACACATGGGGCTGGCAGCGCAGGG 219
QY 149 AGCCGGTGATG 159
DB 220 AGCAGGGCATG 230

RESULT 7
US-09-949-016-133049
Sequence 133049, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 133049
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-133049

Query Match
Best Local Similarity 3.1%; Score 33.4; DB 4; Length 601;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGAGGCAAGATCAACTTAAGAGCCGTTGATCTTAACCATCATCAAGCGCTCAGAA 88
DB 100 TTGCTGTCCTTTGGAAAGTCATTTGCACTGATGACACAAAGGCTCATCTCTGAA 159
QY 89 AGCTGCAAACTTCAAGCCTTTCCAGTAATCCCAAGAGAGCTGTGAGCCCAAGCGG 148
DB 160 TCGTCACTCTGCAGAAAGCAGAAAGGCGCATTCACACATGGGGCTGGCAGCGCAGGG 219

QY 149 AGCCGGTGATG 159
DB 220 AGCAGGGCATG 230

RESULT 8
US-09-949-016-15489/c
Sequence 15489, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15489
LENGTH: 34068
TYPE: DNA
ORGANISM: Human
US-09-949-016-15489

Query Match
Best Local Similarity 3.1%; Score 33.4; DB 4; Length 34068;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGAGGCAAGATCAACTTAAGAGCCGTTGATCTTAACCATCATCAAGCGCTCAGAA 88
DB 16953 TTGCTGTCCTTTGGAAAGTCATTTGCACTGATGACACAAAGGCTCATCTCTGAA 16894
QY 89 AGCTGCAAACTTCAAGCCTTTCCAGTAATCCCAAGAGAGCTGTGAGCCCAAGCGG 148
DB 16893 TCGTCACTCTGCAGAAAGCAGAAAGGCGCATTCACACATGGGGCTGGCAGCGG 16834
QY 149 AGCCGGTGATG 159
DB 16833 AGCAGGGCATG 16823

RESULT 9
US-09-949-016-12559/c
Sequence 12559, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12559
LENGTH: 51711
TYPE: DNA
ORGANISM: Human
US-09-949-016-12559

Query Match 3.1%; Score 33.4; DB 4; Length 51711;
Best Local Similarity 53.4%; Pred. No. 27;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGCAGGCAAGATCAACTCTAAGAGCCGTTGATCTTAACATCAACGCGCTCAGAA 88
DB 34596 TTGCTGTCCCTTTGGAAAGTCCATTTGCCACTGATGGACAAAGGCTCATCTCTGTA 34537
QY 89 AGGTGAAACTTCAAGACCTTTCCAGTAATCCCACTGATGCTTCAGACCCCAAGGCGG 148
DB 34536 TCGTACTCTGCAAGAGCAAGAGGCGCATTCACACTGGGCGTGGCAGCAGAGG 34477
QY 149 AGCCGCGTATG 159
DB 34476 AGCAGGCGCATG 34466

RESULT 10
US-09-252-991A-8192
Sequence 8192, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8192
LENGTH: 2127
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: unsure
LOCATION: (291)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-8192

Query Match 3.1%; Score 33; DB 4; Length 2127;
Best Local Similarity 49.2%; Pred. No. 5.5;
Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 111 CCAAGTAATCCACAGTGTCTGAGCCCAAGGCGGAGCGGTGATGCGGCTTTTC 170
DB 70 CCAAGCTGAACAGCTGAGGCTTATGACAGACGACGCCACCGGAGAGGCTTGAGACCC 129
QY 171 AATGCTTTAGCTCCACCGCTTTGACAGACCAACCATTAAGAGACTTGAATAAGA 230
DB 130 AATACCGGACCCGCGATGCGCATTAACAGAACACCCCTGAAGGCGGAGCGGACCG 189
QY 231 CCGTACACGAAAGTTGAAGAGAGGAGAGATACGATGCTGCCAGCTGTGC 287
DB 190 TCGTGTCTGAAGACTTCACTATGCGCGAAGATCAACCCACTTGCACCAAGAGCGC 246

RESULT 11
US-09-252-991A-8112/c
Sequence 8112, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8112
LENGTH: 2874
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: unsure
LOCATION: (2266)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-8112

Query Match 3.1%; Score 33; DB 4; Length 2874;
Best Local Similarity 49.2%; Pred. No. 6.5;
Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 111 CCAAGTAATCCACAGTGTCTGAGCCCAAGGCGGAGCGGTGATGCGGCTTTTC 170
DB 2487 CCAAGCTGAACAGCTGAGGCTTATGACAGACGACCGCACCGGAGAGGCTTGAGCAC 2428
QY 171 AATGCTTTAGCTCCACCGCTTTGACAGACCAACCATTAAGAGACTTGAATAAGA 230
DB 2427 AATACCGGACCCGCGATGCGCATTAACAGAACACCTGAAGGCGGAGCGGACCG 2368
QY 231 CCGTACACGAAAGTTGAAGAGAGGAGAGATAGGATGCTGCCAGCTGTGC 287
DB 2367 TCGTGTCTGAAGACTTCACTATGCGCGAAGATCAACCCACTTGCACCAAGAGCGC 2311

RESULT 12
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "a" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 3.1%; Score 32.8; DB 3; Length 4403765;
Best Local Similarity 59.8%; Pred. No. 2.8e+02;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 133 CTCGAGCCCAAGGCGGAGCGGTGATGCGGCTTTTCAATGCTCTTGTGCTCACCGTCT 192
DB 3941480 CTCGCGGACAGAGCGGCGCGGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCA 3941539
QY 193 TCGACAGACCAACCATTAAGAGAGCTTGCAC 224
DB 3941540 TCGGCGGACACCGGCGGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3941571

RESULT 13
US-09-632-098-5
Sequence 5, Application US/09632098
Patent No. 6420154


```
;; GENERAL INFORMATION:
;; APPLICANT: Sheppard, Paul O.
;; APPLICANT: Baidur, Nand
;; APPLICANT: Bishop, Paul D.
;; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
;; FILE REFERENCE: 99-39
;; CURRENT APPLICATION NUMBER: US/09/632,098
;; CURRENT FILING DATE: 2000-08-02
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 5
;; LENGTH: 2406
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Degenerate sequence
;; NAME/KEY: misc feature
;; LOCATION: (1) ... (2406)
;; OTHER INFORMATION: n = A,T,C or G
;; 9-632-098-5

Query Match
Best Local Similarity 3.0%; Score 32.2; DB 3; Length 2406;
Matches 82; Conservative 47; Mismatches 197; Indels 0; Gaps 0;

QY 637 CTGCGCGAAGAGATGATCGATGCGCTATTCATCAACGCAATGATTCGAGCGTC 696
Db 1016 CNGCNGCNAACATGCGNCAYGARATHGNCAYMSNTGNGNTMNSNCAYGCCNAYG 1075
QY 697 GAGCTTTCTTCTTGATTCACAAATCGCTGCTCGATCAATCAGCTTCACTTAACT 756
Db 1076 GNTGYGTGNGARGCNGCNGCNGARMSNGNGNTGTATGCGCNGCNGCNGCNGC 1135
QY 757 TTTCCCGCGCGCTGCTTCCGCGCTTCACTGCTGCTTCAACAGGCTTCCAGC 816
Db 1136 AYCCTTTCCNGMGNTTTCGCTTCACTGCTGCTTCAACAGGCTTCCAGC 1195
QY 817 ATGCTAGACCACTCTTCACTTCAAGTTGTTCAAGCAGCGCTTGTATCGTTCAAGC 876
Db 1196 ARGNGNGNGCNGNTGYTMSNAAYGCCNCAVCCNGNTCCNGTCCNGCNGCNY 1255
QY 877 GTTACCGGTTGCAATTTATCAAGAGCAGCGCTTATGCTCCGAGCTCAAGCTCAGGC 936
Db 1256 TWTGYNAAAGNTTGTGARGCNGNGARARGTGYATGCGCNGCNGCNGARART 1315
QY 937 GTAACACCGGAGTTCATCGTCAAT 962
Db 1316 GYMGNGAYTNTGYTGTTCNCAY 1341

RESULT 14
US-10-177-308-5
;; Sequence 5, Application US/10177308
;; Patent No. 6762044
;; GENERAL INFORMATION:
;; APPLICANT: Sheppard, Paul O.
;; APPLICANT: Baidur, Nand
;; APPLICANT: Bishop, Paul D.
;; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
;; FILE REFERENCE: 99-39
;; CURRENT APPLICATION NUMBER: US/10/177,308
;; CURRENT FILING DATE: 2002-06-21
;; PRIOR APPLICATION NUMBER: US/09/632,098
;; PRIOR FILING DATE: 2000-08-02
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 5
;; LENGTH: 2406
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Degenerate sequence
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;; NAME/KEY: misc feature
;; LOCATION: (1) ... (2406)
;; OTHER INFORMATION: n = A,T,C or G
;; US-10-177-308-5
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Best Local Similarity 3.0%; Score 32.2; DB 4; Length 2406;
Matches 82; Conservative 47; Mismatches 197; Indels 0; Gaps 0;
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Db 1076 GNTGYGTGNGARGCNGCNGCNGARMSNGNGNTGTATGCGCNGCNGCNGCNGC 1135
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Db 1196 ARGNGNGNGCNGNTGYTMSNAAYGCCNCAVCCNGNTCCNGTCCNGCNGCNY 1255
QY 877 GTTACCGGTTGCAATTTATCAAGAGCAGCGCTTATGCTCCGAGCTCAAGCTCAGGC 936
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;; Sequence 6, Application US/09632098
;; Patent No. 6420154
;; GENERAL INFORMATION:
;; APPLICANT: Sheppard, Paul O.
;; APPLICANT: Baidur, Nand
;; APPLICANT: Bishop, Paul D.
;; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
;; FILE REFERENCE: 99-39
;; CURRENT APPLICATION NUMBER: US/09/632,098
;; CURRENT FILING DATE: 2000-08-02
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 6
;; LENGTH: 2439
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Degenerate sequence
;; NAME/KEY: misc feature
;; LOCATION: (1) ... (2439)
;; OTHER INFORMATION: n = A,T,C or G
;; US-09-632-098-6
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Query Match
Best Local Similarity 3.0%; Score 32.2; DB 3; Length 2439;
Matches 82; Conservative 47; Mismatches 197; Indels 0; Gaps 0;
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Job time : 220.069 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 07:18:54 ; Search time 673.078 Seconds
(without alignments) 9428.583 Million cell updates/sec

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Perfect score: 1071

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Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	448	41.8	460	9	US-09-924-035A-502
4	439	41.0	453	9	US-09-770-444-615
5	228.6	21.3	1847	17	US-10-424-599-109777
6	185	17.3	185	9	US-09-770-696-257
7	183.6	17.1	1090	17	US-10-425-114-8512
8	157.8	14.7	1176	17	US-10-425-114-14614
9	145.2	13.6	1176	17	US-10-424-599-43464
10	144.8	13.5	1616	18	US-10-739-930-3143
11	138	12.9	1594	17	US-10-424-599-63594

12	129	12.0	1519	17	US-10-425-114-14605	Sequence 14605, A
13	129	12.0	1728	10	US-09-934-455-169	Sequence 169, App
14	129	12.0	1728	10	US-10-225-068-165	Sequence 165, App
15	129	12.0	1728	17	US-10-374-780A-219	Sequence 219, App
16	127.4	11.9	671	17	US-10-374-780A-1390	Sequence 1390, App
17	126	11.8	587	18	US-10-021-323-15482	Sequence 15482, A
18	124.6	11.6	1231	17	US-09-934-455-137	Sequence 137, App
19	124.6	11.6	1231	17	US-10-225-068-245	Sequence 245, App
20	124.6	11.6	1231	17	US-10-302-267-61	Sequence 61, App
21	124.6	11.6	1231	17	US-10-374-780A-2425	Sequence 2425, App
22	124.6	11.6	1231	17	US-10-412-699B-553	Sequence 553, App
23	124.6	11.6	1540	17	US-10-425-114-12989	Sequence 12989, A
24	124.4	11.6	1440	18	US-10-767-795-1247	Sequence 1247, App
25	122.8	11.5	938	18	US-10-767-795-1984	Sequence 1984, App
26	121.6	11.4	1604	15	US-10-295-403-147	Sequence 147, App
27	121.6	11.4	1604	17	US-10-412-699B-551	Sequence 551, App
28	119.8	11.2	587	17	US-10-425-114-30404	Sequence 30404, A
29	119.8	11.2	668	17	US-10-425-114-27401	Sequence 27401, A
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33	117.4	11.0	390	11	US-09-732-627A-4287	Sequence 4287, App
34	113.8	10.6	1260	18	US-10-437-963-26590	Sequence 26590, A
35	113.2	10.6	600	18	US-10-767-795-3868	Sequence 3868, App
36	113	10.6	1322	18	US-10-437-963-12388	Sequence 12388, A
37	111.8	10.4	563	18	US-10-767-701-117	Sequence 117, App
38	111.4	10.4	1608	17	US-10-425-114-8860	Sequence 9860, App
39	111.4	10.4	1830	17	US-10-424-599-79271	Sequence 79271, A
40	111.2	10.4	422	9	US-09-770-423-332	Sequence 332, App
41	111.2	10.4	881	17	US-10-425-114-14725	Sequence 14725, A
42	111.2	10.4	1009	10	US-09-934-455-133	Sequence 133, App
43	111.2	10.4	1009	15	US-10-295-403-145	Sequence 145, App
44	111.2	10.4	1009	15	US-10-278-536-203	Sequence 203, App
45	111.2	10.4	1009	17	US-10-225-068-135	Sequence 135, App

ALIGNMENTS

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RESULT 1
US-09-938-842a-1034
; Sequence 1034, Application US/0993842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1034
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842a-1034
Query Match 100.0%; Score 1071; DB 9; Length 1071;
Best local similarity 100.0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGGCGACATTGAGAGCTTGAAGAGTTGACGCAAGATCAAACTCTTAAGACCGTT 60
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Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Hong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIORITY DATE: 2000-08-24
PRIORITY APPLICATION NUMBER: US 60/227,866
PRIORITY FILING DATE: 2000-01-16
PRIORITY APPLICATION NUMBER: US 60/300,111
PRIORITY FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1034
LENGTH: 1071
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842a-1034

Query Match 100.0%; Score 1071; DB 11; Length 1071;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 109777
; LENGTH: 1847
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MKT3847_70141C.1
US-10-424-599-109777

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Best Local Similarity 62.7%; Pred. No. 5e-67; Indels 18; Gaps 2;

Matches 398; Conservative 0; Mismatches 219; Indels 18; Gaps 2;
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Qy 256 GAGAGAGAGATAGCGATGCTGCAAGTGTGCGGCTAGAGATTTTCAATTAACTGAGAG 315
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Qy 316 TTAAGTCAAAATCCGACGCGCGAAAGATTCGTTGTTTGAAGAGCGTGAAGCGCGC 375
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Db 569 ATATGCGCGCGCGCGAGCGGACAGTCCCGCATGCGAGTGTCCGTAAATGAGAGC 628
Qy 436 TTAATAATCCGACGAGAGAGCGTATTTCTGATATGAGTGAATAATCTGATGAAGAG 495
Matches 436; Conservative 0; Mismatches 219; Indels 18; Gaps 2;

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Qy 496 AAAGTAAACAGACTTCTTAACAGTATATAGACATAA---GCAAGCGCTTTAGCT 552
Db 689 AAGGCAAAACAGACCGGAGATAGCGCTTACGTGAATTAACGCGCGCGCTTTCGTC 748
Qy 553 TCCTCCGCTTAAAGTCCAAATTCGACAGACAGACATCAACCTCCGAGCTTCGCA 612
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Db 809 ACAGCAACATGGAATTCGCAACATACAGCAATTCGCTGCGAAGAAATGCTCC 868
Qy 658 ATGAGGCTTTTCATCAACAGCAATGATCCGAGCTTCGAGCTTCTTCTTATGCTCA 717
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Qy 718 CAATGCTGTCGCTGCAATGAGCTTCAGCTTATT 752
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; Sequence 257, Application US/09770696
; Patent No. US20010044940A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2031US (PARA-020PRV)
; CURRENT APPLICATION NUMBER: US/09/770,696
; PRIOR APPLICATION DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,278
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-696-257

Query Match 17.3%; Score 185; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.3e-52; Indels 0; Gaps 0;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 GCAAGATCAAACTTAAGCGCTGATTAACATCATCAACGCGCTGAGAAAGTGC 94
Db 1 GCAAGATCAAACTTAAGCGCTGATTAACATCATCAACGCGCTGAGAAAGTGC 60
Qy 95 AAATTCAGAGCTTTTCAAGTAAATCCACAGTGAAGTCTGAGCGCCAGAGCGCGCG 154
Db 61 AAATTCAGAGCTTTTCAAGTAAATCCACAGTGAAGTCTGAGCGCCAGAGCGCGCG 120

QY 155 TGATGCCGCGTTTCAATGCTTTAGCTCAACCGCTTCGACAGACCAACCATTTGAAGA 214
DB 121 TGATGCCGCGTTTCAATGCTTTAGCTCAACCGCTTCGACAGACCAACCATTTGAAGA 180
QY 215 GAGCT 219
DB 181 GAGCT 185

RESULT 7
US-10-425-114-8512
Sequence 8512, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingtong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8512
LENGTH: 1090
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700756889_FLI
US-10-425-114-8512

Query Match 17.1%; Score 183.6; DB 17; Length 1090;
Best Local Similarity 63.7%; Pred. No. 1.2e-51;
Matches 320; Conservative 0; Mismatches 164; Indels 18; Gaps 2;

QY 269 GAGTCCCTGCGACGCTGTCGCGCTAGATTTTCAATTAATCTGAGAGTAGGTACAAAT 328
DB 1 GAATCCCGCCGACGCTGTCGCGCTAGATTTTCAATTAATCTGAGAGTAGGTACAAAT 60
QY 329 CCGAGCGGGAACGATTCGCTGCTTTGAGAACGCTACCGCGGATTAAGCCGCA 388
DB 61 CCGAGCGGGAACGATTCGCTGCTTTGAGAACGCTACCGCGGATTAAGCCGCA 120
QY 389 CCGGTAACGGGAACGTTCCCGCATCGCATGTCGCTTAACGGAACCTTAATAATCCGA 448
DB 121 CCGGTAACGGGAACGTTCCCGCATCGCATGTCGCTTAACGGAACCTTAATAATCCGA 180
QY 449 CGACGACGAAACGCTGATTTGATATGAGTGAATATGTAAGAAAGAAACGTAACGAC 508
DB 181 CAACCTCACTTCGATCAAGAACCCGAGAGCCGCCGAGAGAAAGAACGCAACGAC 240
QY 509 CTTTCAACGATGATATATAGACATTA---GGAGCCCGTTTCACTTCTCCGCTTGA 565
DB 241 CCGCGAATAGCCCTTACGTCGACATTAACGCGCCGCCCTTTGCTGCGCCGCGCTG 300
QY 566 CTCGAATTCGACGACGACGACGATCCGCACTCGCACTCGCATCATCATCTGTCG 625
DB 301 CAAGCTCTATTATTAATTAATTAACCAAAACGACGACGACGACGACGACGATG 360
QY 626 CTCAGCACTTC-----TCCCGCAAGAAATGATCCGATGCGGCTATTTC 670
DB 361 CAATTCGCAATACAGCAATTCGCTGCGCGAAGAAATGTTCCGATGCGGCTATCC 420
QY 671 CATTCAACGCAATGATTCGAGCGCTGCGCTTCTTCTGATTCACAAATGCTGCTG 730
DB 421 CTTCAACGCGCGCTTCCGCTGCGAGAGCTTTTGTGTCTCTCAAAACGCGCTGCT 480
QY 731 CCGTCAATCAGCTCAGTTATT 752

DB 481 TTCAGCATCAACCTCAGTTT 502

RESULT 8
US-10-425-114-14614
Sequence 14614, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingtong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 14614
LENGTH: 1176
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: Clone ID: LIB23-065-D10_FLI
US-10-425-114-14614

Query Match 14.7%; Score 157.8; DB 17; Length 1176;
Best Local Similarity 75.9%; Pred. No. 9.3e-43;
Matches 195; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 195 GACAGACCAACCATTTGAAGAGCTTCACTTAAGACCGTCAACAGAGGTTGAAGAG 254
DB 278 GACTTAACCGCTCCGAGAGACCGACTTAAGACCGTCAACAGAGGTTGAAGAG 337
QY 255 AGGAGAAAGATACGATGCTGCGACGCTGCGCTGAGATTTTCAATTAATCTGAGA 314
DB 338 AGGTGAGAGATCCGAATGCGCGCGGTTGCGCTGCTTCAATTAATCCGCTGA 397
QY 315 GTTAGTCAAAATCGACCGCGGAATTCGATGCTGTTGAGAAACGCTGACCGGC 374
DB 398 ACTTGTCACAAATCGACCGGAATTCGATGCTGTTGAGAAACGCTGACCGGC 457
QY 375 GATTATAGCCGACGAGGTAAGGAAACGTTCCCGCATCGCATGCTGTTAAGGAAAC 434
DB 458 GATTAATTGAAGCAACCGGAACCGAACTGTACCGGCTATTGCTGATCGTTAAGGAAAC 517
QY 435 CTTAAATAATCCGACGA 451
DB 518 TTTAAATAATCCGACGA 534

RESULT 9
US-10-424-599-43464
Sequence 43464, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 43464
LENGTH: 1113
TYPE: DNA
ORGANISM: Glycine max
FEATURE:

TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (106)...(1575)
US-10-225-068-165

Query Match 12.0%; Score 129; DB 17; Length 1728;
Best Local Similarity 71.0%; Pred. No. 9,6e-33;
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 189 GTCTTGAAGAGACCACTTGAAGAGCTTCACTAAAGCCCTCAACGAAAGTTGA 248
DB 420 GGCAGCTAATAAGCCACGCTTGAACGAGCGTCGACGAAAGCCGACACAGAAAGTTGA 479
QY 249 AGGAAGAGGAGAGAGATACGATGCTGCGACGATGCGGCTTGAATTTTCAATTAAAC 308
DB 480 CGGAAGAGGAGAGAGATACGATGCTGCGACGATGCGGCTTGAATTTTCAAGCTAAC 539
QY 309 TCGAGAGTTAGTCACTCAATCCGACGCGGAAACGATTGCGTGTGTTGAGAAAGCTGA 368
DB 540 GCGAAGAGTAAAGTCACTCAATCCGACGCGGAAACGATTGCGTGTGTTGAGAAAGCTGA 599
QY 369 GCCGCGATTATAGCCGCGACGCGGTAACGCGGTAACGCGGTAACGCGGTAACGCGGTAAC 428
DB 600 ACCATCTGTAATGCGCGCGACCGGAAACGAAACGAAACGAAACGAAACGAAACGAAACG 659
QY 429 C 429
DB 660 C 660

RESULT 15

US-10-374-780A-219
Sequence 219, Application US/10374780A
Publication No. US2004001927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddie, James
APPLICANT: Brown, Pierre E
APPLICANT: Pilgrim, Marsha L
APPLICANT: Duddell III, Arnold T
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MRI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068

PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 219
LENGTH: 1728
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1064
US-10-374-780A-219

Query Match 12.0%; Score 129; DB 17; Length 1728;
Best Local Similarity 71.0%; Pred. No. 9,6e-33;
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 189 GTCTTGAAGAGACCACTTGAAGAGCTTCACTAAAGCCCTCAACGAAAGTTGA 248
DB 420 GGCAGCTAATAAGCCACGCTTGAACGAGCGTCGACGAAAGCCGACACAGAAAGTTGA 479
QY 249 AGGAAGAGGAGAGAGATACGATGCTGCGACGATGCGGCTTGAATTTTCAATTAAAC 308
DB 480 CGGAAGAGGAGAGAGATACGATGCTGCGACGATGCGGCTTGAATTTTCAAGCTAAC 539
QY 309 TCGAGAGTTAGTCACTCAATCCGACGCGGAAACGATTGCGTGTGTTGAGAAAGCTGA 368
DB 540 GCGAAGAGTAAAGTCACTCAATCCGACGCGGAAACGATTGCGTGTGTTGAGAAAGCTGA 599
QY 369 GCCGCGATTATAGCCGCGACGCGGTAACGCGGTAACGCGGTAACGCGGTAACGCGGTAAC 428
DB 600 ACCATCTGTAATGCGCGCGACCGGAAACGAAACGAAACGAAACGAAACGAAACGAAACG 659
QY 429 C 429
DB 660 C 660

Search completed: February 28, 2005, 12:00:32
Job time : 676.078 secs

Query Match	3.6%	Score 59.8	DB 4	Length 1141
Best Local Similarity	10.5%	Pred. No. 5.8e-06		
Matches	85	Conservative 299	Mismatches 422	Indels 3
Gaps				1
Dy	855	TCGATTACTTGATCTGATTTCTAGTTCGGTGTGTATGTTAATATCCGATTTGACAAG	914	
Db	1002	TNNAMWATTTATWMAYYAAAKAWARWGNMRRWYGAAAGKMGMAAMAATGGBWAATAGKMC	943	
Qy	915	TACACAATGTCATAGTATGCGTATATGATGTGACCGGTTATTCACAAGACGCGACAT	974	
Db	942	NNNNNNTTTIVRRAMAKANNNNNAWTCACYNRAATNNKATITWMMKTHGAHSKRRRH	883	
Qy	975	AGGAGATTTTGGATTCCTGGAAAGAGATTAATTCATAGACACTAAATTAGCTTTTGGT	1034	
Db	882	HTTRCRRTKYNNNNNNNARVTYVWHHAARWMAWMTRTNNNNNNNNNACHRTRTWABW	823	
Qy	1035	GGCGACACCTTGACCTACATTAAATGGGGTCCACCCCAAGTATGGGCTTACAGCTTTT	1094	
Db	822	KHSHCNNNNNNNNNNNNNNTWCHATTANABCYRPAANNNAARARACNNMHAAVITH	763	
Qy	1095	TCCATAAATTAAGAATAATCTTTTGGCTACACATATAAATTAATGAAAAATCTT--	1152	
Db	762	TDMCYKTMWNTTMYMDMTTBTBTTTTRMTTSTNNNNNNNNMMACCTNNNNNNMMKAYAAH	703	
Qy	1153	-TCCAACCATAGAAAGTTAAATTTGATCGACGTGAAATTTTGTGACAAAGCTAGTA	1211	

Best Local Similarity 11.1%; Pred. No. 0.054;
Matches 69; Conservative 227; Mismatches 324; Indels 1; Gaps 1;

```
QY 799 GAATCAAAATTAAGTTGAATCGGTTACATCTAGTACCGTCAATTAATCAATTCATTGCA 858
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 208 RNMYGMBWMKXNSYDTYYWVWMDCKKRVKRWVTRGRMRNRYVAVTAHRRRNNGM 267
QY 855 TTACTTTGATCTGATTTTCAGTTCCGTTTGATGTTTAATCCGATTTGCAATGACA 918
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 268 TAAAYVRRATNNNNNNAAMCKRKYKGMNRAVNSTCTTWSKTTKVITSCWANNGCA 327
QY 919 CAAGTACATAGTATCGGTATATGTATGACCGGTTATCAAGAGAGAGAGAGATAGCA 978
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 328 GDAANDHKMKXKMSAMGVVNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 387
QY 979 GGAATTTGGAATCTCGGAAGAAGATTATTCATAGACACTAATTAAGCTTTTGGTGCG 1038
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 388 KMTBYRKTMVNNNNNGTTWKKMMAVYKMDMDMBGTNNNNNGRTYYGWTNKMKMTY 447
QY 1039 CAGCCTTGACCTACATTAATGGGGTCCAAACCCCAAGTATGGGCTTACAGCTTTTCCA 1098
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 448 YMKKANNCKWRAMDHTCTHNNNTTWKMKTYNNNNNNNNNNNNNNNNNNNNNNNNNNNN 507
QY 1099 TAAATTAAGTAAATCTTTTTCGCTACCAATTAATTAATTAATTAATTAATTAATTA 1158
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 508 RRYAHANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 567
QY 1159 CATGAAAAGTTAAATTTGATCAGCAGTGAATTTTGTACAAAGCTAGTATTTTCA 1218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 568 SPTSRSGRANNYARABHYGVKNTTRWMBWBSHTWBHRAAAYHMMBMBACHCKWAVY 627
QY 1219 T-CGAGGTCTACTAGTAAGTAACTAAGTAACTAAGTAACTAAGTAACTAAGTAACT 1277
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 628 KAKKYTAGAGSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 687
QY 1278 GAAGCTTTCTTAAAGTTAAACAACTATTAATTAATTAATTAATTAATTAATTAAT 1337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 688 YTHANNWCGCMNADTRTRTKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 747
QY 1338 TGAAGAGAGAAATTAAGTTTACTGACCCCATTTGACAGATGCTCCCATTAATTA 1397
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 748 HMRWANKMAMRGHADAAABTTDKRNNGAVTKYTTNNNNNTYGVVTTAARDGMANNNN 807
QY 1398 TAGAAGATAGACCAATGCAA 1418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 808 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 828
```

Query Match 2.6%; Score 44.4; DB 4; Length 832;
Best Local Similarity 14.4%; Pred. No. 0.068;

Matches 50; Conservative 153; Mismatches 144; Indels 1; Gaps 1;

```
QY 10 TTTTACTATGTTTATATGCAAGAGAAATATGCGATGTTGGAAATGCTTTTTCAGA 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 37 YMRMRKKKKAAWKKWKTWMTWYVAMNGYTKKAAKCHTKKKKKKKKKKKKKKKKKKK 96
QY 70 TCATCAAAAGGCTCTACAGATTTCTTGAAGATGTTTCAGCTTTTGTAGAAAATGTG 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 97 SYMAWTTWTGYAYYRSMYMMWRKCKKAYKTKTCYSKGTWMMKMKAAWTTWMM 156
QY 130 TTTATTTGCAACAGTAGAAGACATACATAGACAGATGTATCTAGAGATTAAGCTTT 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 157 KTYWMAATRYWMMACMTKRMFASWYCMWMMGKAKMSTWRSRSYASARCCYSCS 216
QY 190 CTATGCTTAAGAAATGGA-CCGATACGAATTAACCAAGCATTAAGATTAATGCT 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 WGAWSMKYWRWRWRGATGAGMAMPASCMWRKKRYAGKSTYSKSMWCMTRSKYCY 276
QY 249 TTGTAGAAATCTACACTTATTTATGTGAATTTGTGTTAGTGAAGTAAATCAAT 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 TTAATGTGYCYKGGMGKRGKRWYASKKYMMKRWMMWCAWRYRYSGTTPASMMWRMYT 336
QY 309 CGGAATCCAAAACCTCAATTTTACCAATCAGCCCAATTAATTAATGCT 356
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 MAMKMKYAMAPAAWRMMWMMWMBRACAAATATATTAATTAATGCT 384
```

RESULT 5

US-09-790-988-1
Sequence 1, Application US/09790988
Patent No. 6632935
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEKI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
TYPE: DNA
ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 2.6%; Score 43.4; DB 4; Length 640681;
Best Local Similarity 50.2%; Pred. No. 1.9; Mismatches 106; Indels 0; Gaps 0;

```
QY 1146 AATCTTTCACATAGAAAAGTTAAATTTGATCAGCAGTGAATTTTGTACAAAGC 1205
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223591 AATATATATTTATTTATTAACATTTTACATTTTAAATCAATTAATTAATTA 223650
QY 1206 TAGGATTTTCATTTGGAGGTGACTAGTACTAGTAACTAGTAACTAGTAACTAGT 1265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223651 TATATATTTAATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTAA 223710
QY 1266 ATTTTGAATTTGAAGCTTTTCTAGTTTAAACAACTATTTACTTAACTAAAG 1325
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223711 AGCATTTCAATTAATTTTATTTTAAAGTTAAATTAATTTGTAATTAATTTT 223770
QY 1326 AAAAATTTTGTGAAGAAAGAAATTAAGTTTA 1358
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223771 ATTTTATCTAATCGTTAAATATATATTAATGTA 223803
```

RESULT 6
US-09-949-016-12386/c

Sequence 12386, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12386
LENGTH: 263693
TYPE: DNA
ORGANISM: Human
US-09-949-016-12386

Query Match
Best Local Similarity 46.9%; Pred. No. 1.5; Length 263693;
Matches 135; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 1127 AACCATTAATAATTATTAATAATCTTCCACCATAGAAAAGTTAATTGATCAGCGAT 1186
Db 177419 AACCCATTAATAACCTTCTATCTCTAGATATTTGAAAACCTTATTTCTTCTGTC 177360
QY 1187 GGAATTTTGTACAAAGTAGTATTTATTTGGAGTGTACTAGTAAGTATAC 1246
Db 177359 CTGTGTGTTGCTTAACAAATTTTCACTTCAAGTATTTAATAATTTTAAAT 177300
QY 1247 TAACCAAGATGAGTTCTGATTTGATTTGAAGCTTTCTTGGTTAAACAGTA 1306
Db 177299 GAATTAATATGATGTTGCGGAGATTTTCAATCACTAATAATTTGTGCAAGAAATG 177240
QY 1307 TATTACTAAACATTAAGAAAACATTTTGTGAAAAGAAATTAAGTTACTGACCC 1366
Db 177239 TATCTCTAATAATTAATTCATTAATTTTCAAGAAAATTTGATTAATTTTCTAATGCT 177180
QY 1367 CATTTGACAGATGCTCCCATTAATTAATCTGATAGAAATGAGCAATG 1414
Db 177179 ATTTGAAAAGATTAACGTTATTTTGAATATTAATTAATTAACATG 177132

US-09-949-016-16915/c
Sequence 16915, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16915
LENGTH: 263694
TYPE: DNA
ORGANISM: Human
US-09-949-016-16915

Query Match
Best Local Similarity 46.9%; Pred. No. 1.5; Length 263694;
Matches 135; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 1127 AACCATTAATAATTATTAATAATCTTCCACCATAGAAAAGTTAATTGATCAGCGAT 1186
Db 177419 AACCCATTAATAACCTTCTATCTCTAGATATTTGAAAACCTTATTTCTTCTGTC 177360
QY 1187 GGAATTTTGTACAAAGTAGTATTTATTTGGAGTGTACTAGTAAGTATAC 1246
Db 177359 CTGTGTGTTGCTTAACAAATTTTCACTTCAAGTATTTAATAATTTTAAAT 177300
QY 1247 TAACCAAGATGAGTTCTGATTTGATTTGAAGCTTTCTTGGTTAAACAGTA 1306
Db 177299 GAATTAATATGATGTTGCGGAGATTTTCAATCACTAATAATTTGTGCAAGAAATG 177240
QY 1307 TATTACTAAACATTAAGAAAACATTTTGTGAAAAGAAATTAAGTTACTGACCC 1366
Db 177239 TATCTCTAATAATTAATTCATTAATTTTCAAGAAAATTTGATTAATTTTCTAATGCT 177180
QY 1367 CATTTGACAGATGCTCCCATTAATTAATCTGATAGAAATGAGCAATG 1414
Db 177179 ATTTGAAAAGATTAACGTTATTTTGAATATTAATTAATTAACATG 177132

RESULT 8

US-09-949-016-12968/c
Sequence 12968, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12968
LENGTH: 222452
TYPE: DNA
ORGANISM: Human
US-09-949-016-12968

Query Match
Best Local Similarity 49.3%; Pred. No. 2.2; Length 222452;
Matches 138; Conservative 0; Mismatches 141; Indels 1; Gaps 1;

QY 1065 TCACACCCCAAGTAGGCTTACAGCTTTTCATTAATAATTAAGTAATCTTTTTCG 1124
Db 34351 TCTAACATGAATTTGTGTGGAAGATGATTAATTAATAATTTTATTTATTAAT 34292
QY 1125 CTAAACATTAATAATTATTAATAATCTTCCACCATAGAAAAGTTAATTGATCAGCG 1184
Db 34291 ATTAACAAAGAAATTAATTAATAATTTTCAAAATTTAGTAATAACACATTTGAAATCA 34232
QY 1185 ATGGAATTTTGTACAAAGTAGTATTTGATTTGGAGTGTCTAGTAAGTAACT 1244
Db 34231 ATTTGTAATTTTATTTGACTCTTTTATTTGATTTGGAGGAGCAAGAAC-AACCTTTAATTT 34173
QY 1245 ACTAACGAATGAGTTCTGATTTTGGATTTGAAGCTTTCTTGAAGTTAATAAACAAG 1304
Db 34172 ATTAACGAATTTCTTTCTTTTAAACACTGGAATTAAGCTTTTGAAGAAATGGAATTTCT 34113
QY 1305 TATATTTACTAAACATTAAGAAAACATTTTGTGAAAAG 1344
Db 34112 GAAATTTCTAAGAAATGAACTGGAATAATGCTTCAAG 34073

RESULT 9

US-08-076-090-1

Sequence 1, Application US/08076090
Patent No. 5631162

GENERAL INFORMATION:

APPLICANT: Leboulch, Philippe
APPLICANT: London, Irving M.

APPLICANT: Tuan, Dorothy

TITLE OF INVENTION: Retroviral Vectors for Transducing
TITLE OF INVENTION: Beta-Globulin Gene and Beta-Locus Control Region

TITLE OF INVENTION: Derivatives

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kilpatrick & Cody

STREET: 1100 Peachtree Street, Suite 2800

CITY: Atlanta

STATE: Georgia

COUNTRY: U.S.

ZIP: 30309-4530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/076,090

FILING DATE: 19930611

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: MIT 6128

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 815-6508

TELEFAX: (404) 815-6555

INFORMATION FOR SEQ. ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1666 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: Beta-globin gene

FEATURE:

NAME/KEY: misc_signal

LOCATION: 37..298

OTHER INFORMATION: /note= "Exon III"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 299..1148

OTHER INFORMATION: /note= "Intron 2"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 1149..1370

OTHER INFORMATION: /note= "Exon II"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 1371..1501

OTHER INFORMATION: /note= "Intron 1"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 1502..1643

OTHER INFORMATION: /note= "Exon I"

US-08-076-090-1

Query Match

Best Local Similarity 2.5%; Score 42.2; DB 1; Length 1666;

Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Qy	1091	TTTTCCATTAATAAATTAATCTTTTGGCCCAACCAATTAATAATTTGAAATC	1150
Db	684	TGTGTACACATATTTAAACATTACCTTAACCAATTAATGTAATGATTATGATC	743
Qy	1151	TTTCCACCATGAAAGTTAAATTTGATCAGCGATGAAATTTTGTCAAAAGTAGGT	1210
Db	744	AATTGAAATTAAGAAATTAAGTAGGAGATTGAAATGCAAAATAGCACATAT	803
Qy	1211	AATTCATTTGGAGTGTACTAGTAACTAAGTAAGTAAACCAAGATGCTTTGATTTT	1270
Db	804	ATTCCAATATGTAATGACTAGGACAGCTGTAAAGTTTTTTAAAGTTACTTATGT	863
Qy	1271	GGATTTGAGCTTTTCTTACGTTAAACCAAGATATTTACTTAACATTAAGAAAT	1330
Db	864	ATCTCAGAGATATTTCTTTTGTATACCAATGTTAAGGCAATTAAGTAATAGTAA	923
Qy	1331	CATTTGTGAAAGAGAAATTA	1353
Db	924	ATTGGGAGAGAGAAAAAAGA	946

RESULT 10

PCT-US94-06661-1

Sequence 1, Application PC/TUS9406661

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Retroviral Vectors for Transducing

TITLE OF INVENTION: Beta-Globulin Gene and Beta-Locus Control Region

NUMBER OF SEQUENCES: 5

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06661

FILING DATE: 10-JUN-1994

CLASSIFICATION:

INFORMATION FOR SEQ. ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1666 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo Sapiens

CELL TYPE: Beta-globin gene

FEATURE:

NAME/KEY: misc_signal

LOCATION: 37..298

OTHER INFORMATION: /note= "Exon III"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 299..1148

OTHER INFORMATION: /note= "Intron 2"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 1149..1370

OTHER INFORMATION: /note= "Exon II"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 1371..1501

OTHER INFORMATION: /note= "Intron 1"

FEATURE:

NAME/KEY: misc_signal

LOCATION: 1502..1643

OTHER INFORMATION: /note= "Exon I"

PCT-US94-06661-1

Query Match 2.5%; Score 42.2; DB 5; Length 1666;
Best Local Similarity 47.5%; Pred. No. 0.35; Indels 0; Gaps 0;

Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 1091 TTTTCCATAAATTAAGTAATCTTTTGGCTAACCAATTAATTAATGAATC 1150
DB 684 TGTGACACATATTAATAACATTACCTTAACCATTAATATATATATATATATC 743
QY 1151 TTTCCAAACATAGAAAAGTTAATTTGATCAGCAGTGAATTTTGTACAAAGCTAGGT 1210
DB 744 AATTGAAATTAAGAAAATTAAGTACGGAGATTATGAATATGCAATATAGCACATAT 803
QY 1211 ATTTCATTGGAGTGTACTAGTAATAGTACTTAACCAATGATGTTCTGATTT 1270
DB 804 ATTCGAAATATGATATGACTAGCAGACTGTGAAAGTTTTTTTAAGTTACTTAATGT 863
QY 1271 GGAATTTGAAGCTTTTCTTAGTTAAAAACAAGTATTTACTTAACAATTAAGAAAA 1330
DB 864 ATCTCAGAGATATTTCTTTTGTATACCAATGTTAAGCATTAAGTATTAAGTAAAA 923
QY 1331 CATTTTGTGAAAAGAGAAATAAA 1353
DB 924 ATTCGAGAGAGAAAAAAGAA 946

RESULT 11

US-08-550-715-10/C

Sequence 10, Application US/08550715

Patent No. 5750345

GENERAL INFORMATION:

APPLICANT: Bowie, Lemuel J.

TITLE OF INVENTION: Human β -Thalassemia Mutations as a Predictor of

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/550,715

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gase, David A.

REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28493/32834

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: CDS

LOCATION: join(687..778, 909..1131, 1982..2107)

US-08-550-715-10

Query Match 2.5%; Score 42.2; DB 1; Length 2500;

Best Local Similarity 47.5%; Pred. No. 0.41;

Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 1091 TTTTCCATAAATTAAGTAATCTTTTGGCTAACCAATTAATTAATGAATC 1150
DB 1596 TGTGACACATATTAATAACATTACCTTAACCATTAATATATATATATATC 1537
QY 1151 TTTCCAAACATAGAAAAGTTAATTTGATCAGCAGTGAATTTTGTACAAAGCTAGGT 1210
DB 1536 AATTGAAATTAAGAAAATTAAGTACGGAGATTATGAATATGCAATATAGCACATAT 1477
QY 1211 ATTTCATTGGAGTGTACTAGTAATAGTACTTAACCAATGATGTTCTGATTT 1270
DB 1476 ATTCGAAATATGATATGACTAGCAGACTGTGAAAGTTTTTTTAAGTTACTTAATGT 1417
QY 1271 GGAATTTGAAGCTTTTCTTAGTTAAAAACAAGTATTTACTTAACAATTAAGAAAA 1330
DB 1416 ATCTCAGAGATATTTCTTTTGTATACCAATGTTAAGCATTAAGTATTAAGTAAAA 1357
QY 1331 CATTTTGTGAAAAGAGAAATAAA 1353
DB 1356 ATTCGAGAGAGAAAAAAGAA 1334

RESULT 12

US-09-411-449-3/C

Sequence 3, Application US/09411449

Patent No. 6524851

GENERAL INFORMATION:

APPLICANT: James Ellis

TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING

FILE REFERENCE: 17860017

CURRENT APPLICATION NUMBER: US/09/411,449

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 2,246,005

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 3

LENGTH: 3385

TYPE: DNA

ORGANISM: Homo sapiens

US-09-411-449-3

Query Match 2.5%; Score 42.2; DB 4; Length 3385;
Best Local Similarity 47.5%; Pred. No. 0.47;

Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 1091 TTTTCCATAAATTAAGTAATCTTTTGGCTAACCAATTAATTAATGAATC 1150
DB 2128 TGTGACACATATTAATAACATTACCTTAACCATTAATATATATATATATC 2069
QY 1151 TTTCCAAACATAGAAAAGTTAATTTGATCAGCAGTGAATTTTGTACAAAGCTAGGT 1210
DB 2068 AATTGAAATTAAGAAAATTAAGTACGGAGATTATGAATATGCAATATAGCACATAT 2009
QY 1211 ATTTCATTGGAGTGTACTAGTAATAGTACTTAACCAATGATGTTCTGATTT 1270
DB 2008 ATTCGAAATATGATATGACTAGCAGACTGTGAAAGTTTTTTTAAGTTACTTAATGT 1949
QY 1271 GGAATTTGAAGCTTTTCTTAGTTAAAAACAAGTATTTACTTAACAATTAAGAAAA 1330
DB 1948 ATCTCAGAGATATTTCTTTTGTATACCAATGTTAAGCATTAAGTATTAAGTAAAA 1889
QY 1331 CATTTTGTGAAAAGAGAAATAAA 1353
DB 1888 ATTCGAGAGAGAAAAAAGAA 1866

RESULT 13

US-09-710-279-3535

Sequence 3535, Application US/09710279

Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P0348005
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3535
LENGTH: 3386
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-3535

Query Match 2.5%; Score 42.2; DB 4; Length 3386;
Best Local Similarity 51.9%; Pred. No. 0.47;
Matches 95; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1102 AATTAAAGTAATCTTTTGGCTAACCAATATAATTGTAATCTTCCACCAT 1161
DB 1470 ATTAAAGTAAGTTTGTGTAATTAACAGGAAATGTTAAATAGATGTCCAATGA 1529
QY 1162 AGAAAGTAAATTTGATCAGCATGAAATTTTGTACAAAGCTAGATTTGATTGG 1221
DB 1530 ATATAGTAAATTAATTAATCAACAAATTAATGTAATTAACCTCGTTCTAATAATTG 1589
QY 1222 GAGTGTACTAGTACTAGTAAGTACTACCAATGATTTGATTTGGATTGGAAAG 1281
DB 1590 TCGCTTAATTAATCAATATGCGCATNACTGTATTCAGATATCTTTGATATTTTACC 1649
QY 1282 CTT 1284
DB 1650 TTT 1652

RESULT 14
US-09-411-449-1/c
Sequence 1, Application US/09411449
Patent No. 6524851
GENERAL INFORMATION:
APPLICANT: James Ellis
TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING
FILE REFERENCE: 17860017
CURRENT APPLICATION NUMBER: US/09/411,449
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 2,246,005
PRIOR FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 3496
TYPE: DNA
ORGANISM: Homo sapiens
US-09-411-449-1

Query Match 2.5%; Score 42.2; DB 4; Length 3496;
Best Local Similarity 47.5%; Pred. No. 0.47;
Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 1091 TTTTCCATTAATTAAGTAATCTTTTGGCTAACCAATATAATTATGAAATC 1150
DB 2239 TGTGTACACATTAATTAACCTTACCTTTAACCCATTAATATGATATGATATC 2180
QY 1151 TTTCACACATTAAGTAATTTGATCAGCATGAAATTTTGTACAAAGCTAGGT 1210
DB 2179 AATTAAATTAAGTAATTAAGTACGATTAATGCAATATGACACACTAT 2120

QY 1211 ATTTCATTTGGAGTACTAGTAAGTACTAACCAATAGACTTTCTGATTT 1270
DB 2119 ATTCCAAATAGTAATGTAATGTAAGTACTAGTAAAGTTTCTTAACTTATATGT 2060
QY 1271 GGATTTTGAAGCTTTTCTTGTAGTTAAACCAATATATTAACAATTAAGAAAA 1330
DB 2059 ATCTCAGATATTTCTTTGTTATACCAATGTTAAGCATTTAGTAAATAGTAATA 2000
QY 1331 CATTTTGTAAAAAGAAATATA 1353
DB 1999 ATTGCGAGAGAAAAAAGAA 1977

RESULT 15
US-09-411-449-4/c
Sequence 4, Application US/09411449
Patent No. 6524851
GENERAL INFORMATION:
APPLICANT: James Ellis
TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING
FILE REFERENCE: 17860017
CURRENT APPLICATION NUMBER: US/09/411,449
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 2,246,005
PRIOR FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 3805
TYPE: DNA
ORGANISM: Homo sapiens
US-09-411-449-4

Query Match 2.5%; Score 42.2; DB 4; Length 3805;
Best Local Similarity 47.5%; Pred. No. 0.49;
Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 1091 TTTTCCATTAATTAAGTAATCTTTTGGCTAACCAATATAATTATGAAATC 1150
DB 2548 TGTGTACACATTAATTAACCTTACCTTTAACCCATTAATATGATATGATATC 2489
QY 1151 TTTCACACATTAAGTAATTTGATCAGCATGAAATTTTGTACAAAGCTAGGT 1210
DB 2488 AATTAAATTAAGTAATTAAGTACGATTAATGCAATATGACACACTAT 2429
QY 1211 ATTTCATTTGGAGTACTAGTAAGTACTAACCAATAGACTTTCTGATTT 1270
DB 2428 ATTCCAAATAGTAATGTAATGTAAGTACTAGTAAAGTTTCTTAACTTATATGT 2369
QY 1271 GGATTTTGAAGCTTTTCTTGTAGTTAAACCAATATTAACAATTAAGAAAA 1330
DB 2368 ATCTCAGATATTTCTTTGTTATACCAATGTTAAGCATTTAGTAAATAGTAATA 2309
QY 1331 CATTTTGTAAAAAGAAATATA 1353
DB 2308 ATTGCGAGAGAAAAAAGAA 2286

Search completed: February 28, 2005, 08:17:54
Job time : 333.931 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 07:18:54 ; Search time 1053.92 Seconds
(without alignments)
9428.563 Million cell updates/sec

Title: US-09-938-842a-3729

Perfect score: 1677

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Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues 10789606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database :

Published Applications NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	50.6	3.0	8056	18	US-10-473-126-386
4	49.6	3.0	8056	14	US-10-198-846-7035
5	49.2	2.9	3673778	16	US-10-312-841-2
6	49.2	2.9	3673778	16	US-10-312-841-1
7	48.6	2.9	20933	18	US-10-433-793-154
8	47.8	2.9	2958	9	US-09-938-842a-338
9	47.8	2.9	2958	11	US-09-938-842a-338
10	46.6	2.8	516	9	US-09-960-352-5785
11	46.6	2.8	789	17	US-10-282-122a-15640

12	46.4	2.8	610	18	US-10-021-333-8212	Sequence 8212, Ap
13	46.4	2.8	7047	15	US-10-240-453-259	Sequence 259, Ap
14	46.4	2.8	17848	15	US-10-239-676-28	Sequence 28, Appl
15	46.4	2.8	17848	15	US-10-240-453-38	Sequence 38, Appl
16	46.4	2.8	17848	15	US-10-257-166-58	Sequence 58, Appl
17	46.4	2.8	17848	15	US-10-473-166-58	Sequence 38, Appl
18	45.6	2.7	8056	18	US-10-433-793-28	Sequence 28, Appl
19	45.4	2.7	37515	17	US-10-424-599-4304	Sequence 195, Ap
20	45.4	2.7	6352	18	US-10-221-613-195	Sequence 233686
21	45.2	2.7	616	13	US-10-027-632-233686	Sequence 233686
22	45.2	2.7	616	17	US-10-027-632-233686	Sequence 17272, A
23	44.8	2.7	502	10	US-09-814-353-17272	Sequence 2829, Ap
24	44.8	2.7	1271	11	US-09-938-842a-2829	Sequence 2829, Ap
25	44.6	2.7	1271	11	US-09-938-842a-2829	Sequence 4676, Ap
26	44.6	2.7	556	10	US-09-814-353-1676	Sequence 10975, A
27	44.6	2.7	556	10	US-09-814-353-10975	Sequence 4038, Ap
28	44.6	2.7	2000	9	US-09-938-842a-4038	Sequence 4038, Ap
29	44.6	2.7	2000	11	US-09-938-842a-4038	Sequence 6375, Ap
30	44.4	2.6	531	18	US-10-021-323-6375	Sequence 34, Appl
31	44.4	2.6	357652	18	US-10-322-696-34	Sequence 31704, A
32	44.2	2.6	449	17	US-10-424-599-31704	Sequence 424, Ap
33	44.2	2.6	8711	17	US-10-311-455-1906	Sequence 1906, Ap
34	44.2	2.6	19734	15	US-10-311-455-2148	Sequence 2148, Ap
35	44.2	2.6	113515	15	US-10-357-930-7430	Sequence 7430, Ap
36	44	2.6	7498	15	US-10-311-455-230	Sequence 230, Ap
37	43.8	2.6	12643	17	US-10-424-599-4304	Sequence 4304, Ap
38	43.6	2.6	11473	15	US-10-311-455-1328	Sequence 1328, Ap
39	43.6	2.6	11473	17	US-10-257-166-112	Sequence 112, Ap
40	43.4	2.6	6533	15	US-10-240-453-257	Sequence 257, Ap
41	43.4	2.6	7008	17	US-10-221-714A-254	Sequence 254, Ap
42	43.4	2.6	15161	9	US-10-221-613-386	Sequence 386, Ap
43	43.4	2.6	640681	17	US-09-790-988-1	Sequence 1, Appl
44	43.2	2.6	392	17	US-10-621-901-138	Sequence 138, Ap
45	43.2	2.6	2338	14	US-10-198-846-9862	Sequence 9862, Ap

ALIGNMENTS

RESULT 1
US-09-938-842a-3729
; Sequence 3729, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3729
; LENGTH: 1677
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842a-3729

Query Match 100.0%; Score 1677; DB 9; Length 1677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGTAAAGCGTTTACTTATGTTATGCAACGAAAGATATGGCATTTGGCATGC 60

QY 61 TTTTCAGATCATCAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTGTTA 120
 Db 61 TTTTCAGATCATCAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTGTTA 120
 QY 121 GAAATTTGTTTATTCGCAAGGTAGAGAACTATACATAGACAGATGTATCTGAGAGA 180
 Db 121 GAAATTTGTTTATTCGCAAGGTAGAGAACTATACATAGACAGATGTATCTGAGAGA 180
 QY 181 TAAGCTTCTATGTCTAAAGAAATGGAACGATACCAATTAACAAAGCATTAAAGAT 240
 Db 181 TAAGCTTCTATGTCTAAAGAAATGGAACGATACCAATTAACAAAGCATTAAAGAT 240
 QY 241 TAATGCTTTGTAAGAAATCTACACTTATTTATGTAAATTTGTGTAGTGAAGAT 300
 Db 241 TAATGCTTTGTAAGAAATCTACACTTATTTATGTAAATTTGTGTAGTGAAGAT 300
 QY 301 AAAAATCATCGAATCCAAAACCTCAATTTACATCAGCCCAATTTATGATGCTGCG 360
 Db 301 AAAAATCATCGAATCCAAAACCTCAATTTACATCAGCCCAATTTATGATGCTGCG 360
 QY 361 TAATGATGTAATGCTGATGTAGGCAAAAGTTGGTGGTGGCAAAATTAACAATATC 420
 Db 361 TAATGATGTAATGCTGATGTAGGCAAAAGTTGGTGGTGGCAAAATTAACAATATC 420
 QY 421 CCTGTGATGTAATGCTGATGTAGGCAAAAGTTGGTGGTGGCAAAATTAACAATATC 480
 Db 421 CCTGTGATGTAATGCTGATGTAGGCAAAAGTTGGTGGTGGCAAAATTAACAATATC 480
 QY 481 AAGCTTAAAGGTTACTACCGGTTTGAACCGGTTTAAATTTGGTGTAAATCTTAATCC 540
 Db 481 AAGCTTAAAGGTTACTACCGGTTTGAACCGGTTTAAATTTGGTGTAAATCTTAATCC 540
 QY 541 GATTCGGTTGTTTGTATCTCAAGGCAAGTTATGCGCAATATTTGATTTTGAATG 600
 Db 541 GATTCGGTTGTTTGTATCTCAAGGCAAGTTATGCGCAATATTTGATTTTGAATG 600
 QY 601 GATAGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Db 601 GATAGGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 661 AGAGTAAAGGTTACTACCGGTTTGAACCGGTTTAAATTTGGTGTAAATCTTAATCC 720
 Db 661 AGAGTAAAGGTTACTACCGGTTTGAACCGGTTTAAATTTGGTGTAAATCTTAATCC 720
 QY 721 TGCTTAAGGTTGTTTGTATCTCAAGGCAAGTTATGCGCAATATTTGATTTTGAATG 780
 Db 721 TGCTTAAGGTTGTTTGTATCTCAAGGCAAGTTATGCGCAATATTTGATTTTGAATG 780
 QY 781 CCCGAAACAAAGTACCAAGATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 840
 Db 781 CCCGAAACAAAGTACCAAGATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 840
 QY 841 AACTTAACATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Db 841 AACTTAACATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 CCGGATTTGACAGTACCAAGTACATGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 901 CCGGATTTGACAGTACCAAGTACATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 961 AAAGGACGAGTACCAAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Db 961 AAAGGACGAGTACCAAGTACATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 QY 1021 ATTAGCTTTTGGTGGCGAGCTTGTGACTATTAATGAGGTTCAACCCCAAGTATG 1080
 Db 1021 ATTAGCTTTTGGTGGCGAGCTTGTGACTATTAATGAGGTTCAACCCCAAGTATG 1080
 QY 1081 GGCTTAACGCTTTTTCATTAATTAAGTAAATCTTTTGGCTTAACCAATTAATTAAT 1140
 Db 1081 GGCTTAACGCTTTTTCATTAATTAAGTAAATCTTTTGGCTTAACCAATTAATTAAT 1140

QY 1141 ATTGAATCTTTCCAAACCATAGAAAAGTTAAATTTGATCAGGAGTGAATTTTGTAC 1200
 Db 1141 ATTGAATCTTTCCAAACCATAGAAAAGTTAAATTTGATCAGGAGTGAATTTTGTAC 1200
 QY 1201 AAAGTAAAGTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 Db 1201 AAAGTAAAGTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1261 TTCTGATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGAT 1320
 Db 1261 TTCTGATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTGAT 1320
 QY 1321 AAAAAGAAACATTTTGTGAAAAGAAAATAAGTTTACTGACCCCATTTGATGATGATGAT 1380
 Db 1321 AAAAAGAAACATTTTGTGAAAAGAAAATAAGTTTACTGACCCCATTTGATGATGATGAT 1380
 QY 1381 TCCCATTAATTAATCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 Db 1381 TCCCATTAATTAATCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1441 TCGGAATGTTCTTTAAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1441 TCGGAATGTTCTTTAAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 QY 1501 AAAGGTTAAATTAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 Db 1501 AAAGGTTAAATTAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 QY 1561 AACTTAAGTAAATCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Db 1561 AACTTAAGTAAATCTGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1621 GCTTTTAAACATCTTCGTCGTCATCTCAACCGTCCGTTTCTGATGATGATGATGATGAT 1677
 Db 1621 GCTTTTAAACATCTTCGTCGTCATCTCAACCGTCCGTTTCTGATGATGATGATGATGAT 1677

RESULT 2
 US-09-938-842A-3729
 ; Sequence 3729, Application US/09938842A
 ; Publication No. US20040009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: S00-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 3729
 ; LENGTH: 1677
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-3729

Query Match 100.0%; Score 1677; DB 11; Length 1677;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAAAGCTTTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 Db 1 GGTAAAGCTTTTACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 QY 61 TTTTCAGATCATCAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTGTTA 120


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Db 61 TTTTCAGATCATCAAGGCTCTACAGATTTCTTAGGAAATGTTTCAGGGCTTTTGTAA 120
Qy 121 GAAATTTGTTTATTGCAACAGGTAGAGAAACATACATAGACAGATGATCTGAAGAA 180
Db 121 GAAATTTGTTTATTGCAACAGGTAGAGAAACATACATAGACAGATGATCTGAAGAA 180
Qy 181 TAGGCTCTCTATGCTTAAGAAATGAGCCGATAGCAATTAACAGCATCATTAAGAT 240
Db 181 TAGGCTCTCTATGCTTAAGAAATGAGCCGATAGCAATTAACAGCATCATTAAGAT 240
Qy 241 TAAATGTTTGTAGAAATACATACTTATTTATGAAATGTGTGTTAGTGAAGAT 300
Db 241 TAAATGTTTGTAGAAATACATACTTATTTATGAAATGTGTGTTAGTGAAGAT 300
Qy 301 AAAAATATGGAATCCAAACCTCAATTTTACCAATCAGCCCAATTTATGATGCTGGG 360
Db 301 AAAAATATGGAATCCAAACCTCAATTTTACCAATCAGCCCAATTTATGATGCTGGG 360
Qy 361 TAAATGATGATATGCTGATGATAGGCAAAAGTTGGTGGCGGAAATTAACAATTATC 420
Db 361 TAAATGATGATATGCTGATGATAGGCAAAAGTTGGTGGCGGAAATTAACAATTATC 420
Qy 421 CCTGTGTGTGACCCGGAATCTGTAAATCGGAAAGGTGGAACCCACTGTTTAACTTT 480
Db 421 CCTGTGTGTGACCCGGAATCTGTAAATCGGAAAGGTGGAACCCACTGTTTAACTTT 480
Qy 481 AAGCTTAAAGGTACTACCGGTTTGAACGGTTTAAATTTGTTTAACTTAACTTCC 540
Db 481 AAGCTTAAAGGTACTACCGGTTTGAACGGTTTAAATTTGTTTAACTTAACTTCC 540
Qy 541 GATCGCTTGTGTTTAAATCTCAAGGCAAGTTATCGGCAATTTTAAATTTTAAAGT 600
Db 541 GATCGCTTGTGTTTAAATCTCAAGGCAAGTTATCGGCAATTTTAAATTTTAAAGT 600
Qy 601 GGTAGGGAATGTGTGGGTGCAATAGTTGGGCTTACGCTCAACATGTGTGAATGAA 660
Db 601 GGTAGGGAATGTGTGGGTGCAATAGTTGGGCTTACGCTCAACATGTGTGAATGAA 660
Qy 661 AAGATAGGTTCCAGCTCAGGCCCACTTCAATTTTCTGTTTGTAGCTTTCTTTCTG 720
Db 661 AAGATAGGTTCCAGCTCAGGCCCACTTCAATTTTCTGTTTGTAGCTTTCTTTCTG 720
Qy 721 TCGTTACGGTCCCTCTTCTGCGGTGCTGATGTAAGATGATAGCTAGTGGTCAAA 780
Db 721 TCGTTACGGTCCCTCTTCTGCGGTGCTGATGTAAGATGATAGCTAGTGGTCAAA 780
Qy 781 CCCGAAACAAGTACCAACGAATCAAAATAGTTGAATCGTTACATCTAGTTACCGTG 840
Db 781 CCCGAAACAAGTACCAACGAATCAAAATAGTTGAATCGTTACATCTAGTTACCGTG 840
Qy 841 AACTTACATCATTTGATTAATCTTGTATGATCTGATTTCTAGTTGCGTTTGTATAT 900
Db 841 AACTTACATCATTTGATTAATCTTGTATGATCTGATTTCTAGTTGCGTTTGTATAT 900
Qy 901 CCGGATTTGACAGTACCAAGTACATTAAGTATGATGATGATGATGATGATGATGAT 960
Db 901 CCGGATTTGACAGTACCAAGTACATTAAGTATGATGATGATGATGATGATGATGAT 960
Qy 961 AAAAGACGATAGAGAGATTTTGAATCTGAAAAGAGATTTTTCATAGACATA 1020
Db 961 AAAAGACGATAGAGAGATTTTGAATCTGAAAAGAGATTTTTCATAGACATA 1020
Qy 1021 ATTAGCTTTTGTGCGCGAGCTTGTGACATTAATGAGGTCGAACCCCAAGTATG 1080
Db 1021 ATTAGCTTTTGTGCGCGAGCTTGTGACATTAATGAGGTCGAACCCCAAGTATG 1080
Qy 1081 GGGTTACAGCTTTTTCATTAATTAAGTAAATCTTTTTCCTTACCAATTAATTAAT 1140
Db 1081 GGGTTACAGCTTTTTCATTAATTAAGTAAATCTTTTTCCTTACCAATTAATTAAT 1140
Qy 1141 ATTGAATCTTTTCAACCATAGAAAAGTTAAATTTGATCAGGATGAAATTTTGTAC 1200
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Db 1141 ATTGAATCTTTTCAACCATAGAAAAGTTAAATTTGATCAGGATGAAATTTTGTAC 1200
Qy 1201 AAAGCTAGGATTTTGAATTTGGAGTGTACTAGTAATCTAGTAACTAACAGAAATGAT 1260
Db 1201 AAAGCTAGGATTTTGAATTTGGAGTGTACTAGTAACTAGTAACTAACAGAAATGAT 1260
Qy 1261 TTTCTGATTTTGGATTTTGGAGCTTTTCTTAAAGTATTAAGTATTAATTAATTAAT 1320
Db 1261 TTTCTGATTTTGGATTTTGGAGCTTTTCTTAAAGTATTAAGTATTAATTAATTAAT 1320
Qy 1321 AAAAGAAAAATTTTGTGAAAAGAAATTAAGTTTACTGGAACCCCATTTGACAGATG 1380
Db 1321 AAAAGAAAAATTTTGTGAAAAGAAATTAAGTTTACTGGAACCCCATTTGACAGATG 1380
Qy 1381 TCCCAATTAATTAATCTGATGATGAGATGAGCAATGGAAGATGATTTGTCAGGTGACA 1440
Db 1381 TCCCAATTAATTAATCTGATGATGAGATGAGCAATGGAAGATGATTTGTCAGGTGACA 1440
Qy 1441 TCGGAATGTTCTTTTAAAGCTCATGCAACATCAGAACCGTTGATTTTCCCGCATCA 1500
Db 1441 TCGGAATGTTCTTTTAAAGCTCATGCAACATCAGAACCGTTGATTTTCCCGCATCA 1500
Qy 1501 AAAGCTTGAATATCTATCTCACTTGTCTTCTGCTCTATATATATATCTGACGAGTC 1560
Db 1501 AAAGCTTGAATATCTATCTCACTTGTCTTCTGCTCTATATATATATCTGACGAGTC 1560
Qy 1561 AATTTAGTAACTCTCTGAGATGTAACCGGTTAAACGATTTTCCATTTGATCC 1620
Db 1561 AATTTAGTAACTCTCTGAGATGTAACCGGTTAAACGATTTTCCATTTGATCC 1620
Qy 1621 GCTTTTAAACAATCTGTCGTCATCTCCACGCTCGTTTCTCTAGATATTTTAA 1677
Db 1621 GCTTTTAAACAATCTGTCGTCATCTCCACGCTCGTTTCTCTAGATATTTTAA 1677

RESULT 3
US-10-473-126-386
; Sequence 386, Application US/10473126
; Publication No. US2004023493A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match 3 0%; Score 50.6; DB 18; Length 8056;
Best Local Similarity 49.4%; Pred. No. 0.63;
Matches 131; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

Qy 1091 TTTTTCATTAATTAATTAAGTAAATCTTTTTCCTTACCAATTAATTAATTAATTAATC 1150
Db 5627 TTTTTCATTAATTAATTAAGTAAATCTTTTTCCTTACCAATTAATTAATTAATTAATC 1150
Qy 1151 TTTTTCATTAATTAATTAAGTAAATCTTTTTCCTTACCAATTAATTAATTAATTAATC 1210
Db 5687 TTTTTCATTAATTAATTAAGTAAATCTTTTTCCTTACCAATTAATTAATTAATTAATC 1210
Qy 1211 ATTTCATTTGGAGATGATAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACT 1270
Db 5747 TTTTTCATTTGGAGATGATAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACT 1270
Qy 1271 GATTTTGAAGCTTTTCTTAAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1330
Db 5747 TTTTTCATTTGGAGATGATAGTAACTAGTAACTAGTAACTAGTAACTAGTAACTAGTAACT 1270
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Db 5807 TTTATGTTTTTATTTTAAATAATTGAAAAAAATGTTATATAAAAAATAAAAAATA 5866
QY 1331 CATTTCGTAAGAGAAATAAAGT 1355
Db 5867 AAAAAAAAAAAAAAAAAATTTAATT 5891

RESULT 4
US-10-198-846-7035/c
Sequence 7035, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7035
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 137, 182, 183, 184, 185, 186, 187, 188, 209, 211, 212, 217,
LOCATION: 219, 224, 225, 236, 237, 238, 240, 241, 242, 248, 250, 252,
LOCATION: 253, 259, 276, 279, 281, 294, 298, 304, 306, 315, 318, 319,
LOCATION: 320, 321, 327, 338, 349, 350, 352, 355, 363, 378, 379
OTHER INFORMATION: n = A, T, C or G
FEATURE:
NAME/KEY: misc.feature
LOCATION: 380, 386, 389, 393, 398, 400, 408, 410, 414, 434, 441,
LOCATION: 443, 446, 451, 459, 466, 488, 490, 497, 498, 499, 501, 503,
LOCATION: 506, 509, 513, 517, 526, 527, 528, 529, 536, 550, 557, 562,
LOCATION: 564, 565, 573, 576, 588, 599, 604, 607, 616, 617, 619
OTHER INFORMATION: n = A, T, C or G
FEATURE:
NAME/KEY: misc.feature
LOCATION: 627, 628, 643, 649, 661, 668, 672, 680, 689, 698, 706, 719,
LOCATION: 722, 735, 739, 750, 763, 765, 769, 771, 772, 774, 784, 787,
LOCATION: 790, 791, 792, 795, 798, 805, 814, 816, 819, 820, 822, 830,
LOCATION: 832, 833, 838, 842, 847, 849, 850, 853, 856, 857
OTHER INFORMATION: n = A, T, C or G
US-10-198-846-7035

Query Match 3.0%; Score 49.6; DB 14; Length 858;
Best Local Similarity 42.1%; Pred. No. 0.38;
Matches 118; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 1088 AGCTTTTCCATTAATAAGTAATCTTTTGGCTTAACAATAATAATTATGA 1147
Db 382 ATNNNTTGAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 323
QY 1148 ATCTTCCACATAGAAAGTAATTTGATCAGGATGGAATTTTGTACAAAGCTA 1207
Db 322 GNNNNCAAAATTAANTTTTNGTTNAAAAAATAATAATAATAATAATAATAATA 263
QY 1208 GGTATTTCAATTTGGAGTGTACTAGTAAGTAAGTAAGTAAGTAAGTAAGT 1267
Db 262 AAGTTTANNANANATTTNNNANNTAAATTTTNNTAANANTTAANNCTTTT 203
QY 1268 TTGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATTTACTAAACAATAAGAA 1327
Db 202 TTTTATTTTATTAANN 143

QY 1328 AACATTTCGTAAGAGAAATAAGTTTACTGACCC 1367
Db 142 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGTACCTC 103

RESULT 5
US-10-312-841-2/c
Sequence 2, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (379615)
US-10-312-841-2

Query Match 2.9%; Score 49.2; DB 16; Length 3673778;
Best Local Similarity 49.2%; Pred. No. 23;
Matches 129; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 1096 CCATTAATAATAAGTAATCTTTTGGCTTAACAATAATAATAATTATGAATACTTTCC 1155
Db 2005659 CCATTAATACTTAATAAATCCCTTAATCTTAACCCAAAAATTTCCAAACTATTA 2005600
QY 1156 AACATAGAAAGTAATTTGATCAGATGGAATTTTGTCAAGCTAGGATTTTC 1215
Db 2005599 CCACAAACCCAAAGAAAAAATTAATAATAATAATAATAATAATAATAATAATA 2005540
QY 1216 ATTTGGAGTGTACTAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGT 1275
Db 2005539 ATATTAATAACATCTTAATACATTAATAATAATAATAATAATAATAATAATA 2005480
QY 1276 TTGAAGCTTTCTTGTGTTAAAAACAAGTATTTACTTAACAATAATAATAATAATA 1335
Db 2005479 TCATTAATATTAATTAATTAATAATAATAATAATAATAATAATAATAATAATA 2005420
QY 1336 TGTGAAGAGAAATAAGTTT 1357
Db 2005419 ACCAAAAATTAATAATAATAATT 2005398

RESULT 6
US-10-312-841-1/c
Sequence 1, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (3294164)
US-10-312-841-1


```

RESULT 10
US-09-960-352-5785/c
; Sequence 5785, Application US/09960352
; Patent No. US20020137139A1
; SERIAL INFORMATION:
;
; APPLICANT: Waitren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wyatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5785
;
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (76),(90)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1
; US-09-960-352-5785

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RESULT 11
US-10-282-122A-15640

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/ Sequence 15640, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.03A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15640
/ LENGTH: 789
/ TYPE: DNA
/ ORGANISM: Clostridium acetobutylicum
US-10-282-122A-15640

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Query Match	Best Local Similarity	48.08%	Pred. No. 1.8	Score 46.6	DB 17	Length 789
Matches 133	Conservative 0	Mismatches 144	Indels 0	Gaps 0		
QY	1074	AAAGTATGGGCTTACACGCTTTTTCCTAAATAAAGTAATCTTTTGGCCATACCAT	113			
Db	52	AAAAAGCCGCTTAGCTTAGATGATGATATATAATCAAAATGAAATCTTTAATTTAGTTAAG	111			
QY	1134	AAAAATATATGAAATCTTTCCACACCATAGAAAAGTTAAATTTGATCAGCATGGAAT	1193			
Db	112	AGAAATTTAAAGAACCTCTCGAAAAAGAAAATATATCTATTAATACCAAAAATTTAAAAAG	171			
QY	1194	TTTGTGCAACAGCTAAGTATTTCAATTTGGAGGTGACTAGTAACCTAGTAAGTACTAAGCAG	1253			
Db	172	GCATCCACCATTAAGGGAGTTATTAAGGAAAGATTTTAATCCGTAATAAATATAGACAAT	231			
QY	1254	AATGATTTCTGATTTTGATTTTGAAGCTTTTCTTAGTGTAAAAACAAGATATTACT	1313			
Db	232	TATGAAAAATATTAACATGATGACGTGTCATTTCTTAACGAAAAGAAAATATTTTCTGTGGA	291			
QY	1314	AAACATATAAAGAAAACATTTTGTGAAAAGCAAT	1350			
Db	292	AAAAATGAATCACTTTAAGATTTGTAAGAAGAGCACT	328			

RESULT 12
US-10-021-323-8212
Sequence 8212, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
SEQ ID NO 8212
LENGTH: 610
TYPE: DNA
ORGANISM: *Gossypium hirsutum*
FEATURE:
OTHER INFORMATION: Clone ID: LIB828-007-Q1-K6-G2
US-10-021-323-8212
Query Match
Best Local Similarity 2.8%; Score 46.4; DB 18; Length 610;
Best Local Similarity 53.3%; Pred. No. 1.8; Mismatches 86; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 1169 TTAATTTGATGAGCATGGAATTTTGTACAAAGCTAGTATTCATTGGGAGCTGA 1228
DB 152 TTGAGTTCAATGCTAGTATGGAATTTTGTCCAAAGTTGATTTTAATTTCTCATGTT 211
QY 1229 CTAGTACTAGTACTGACCAAGATGATTTGATTTGGATTTGAACTTTTCT 1288
DB 212 ATTAACAACTATGATGGAATTCACATTTATGTTATGTTCTAGTGTATTTATCTTAT 271
QY 1289 TAGGTTAAACCAATATATTTACTTAACCAATTAAGAAAACATTTTGGAAGAAAGAA 1348
DB 272 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 331
QY 1349 ATTA 1352
DB 332 AAAA 335
RESULT 13
US-10-240-453-259
Sequence 259, Application US/10240453
Publication No. US20030148326A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 259

LENGTH: 7047
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (182)
US-10-240-453-259
Query Match
Best Local Similarity 2.8%; Score 46.4; DB 15; Length 7047;
Best Local Similarity 49.7%; Pred. No. 5.6; Mismatches 145; Indels 1; Gaps 1;
Matches 145; Conservative 0; Mismatches 146; Indels 1; Gaps 1;
QY 1084 TTACAGCTTTTCCATTAATTTAAAGTAATCTTTTGGCTTACCATTAATTAAT 1143
DB 3514 TTATATATGATATATGATTAATTTTGAATTTATTTTGAATTTTATTTAGAGAAAT 3573
QY 1144 GAAATCTTTCCACATGAAAGTAATTTGATCAGCATGGAATTTTGTACAA 1203
DB 3574 GAAATTTCCGTTATATTA-AAAATTTGATACGATGTTTATAGATTTATTTGTAA 3632
QY 1204 GCTAGTATTTCAATTTGGAGTGTACTAGTAACATGTAAGTAAACGAAATGAGTTTC 1263
DB 3633 TGTCGAAATTTGATGATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTT 3692
QY 1264 TGATTTGATTTTGAAGCTTTTCTTAGCTTAAACAGATATTTACTTAACATTA 1323
DB 3693 TTATGATTTATTAAGAAATTTGATTTTGAATTTAAATTTGATTTATTTATTA 3752
QY 1324 AGAAACATTTTGTGAAGAAATTAAGTTTCTGAGCCCATTTGTACA 1375
DB 3753 ATTAATTTAAATTTTAAAGGAATTAATTTGATGAGTAAATTAATTTAA 3804
RESULT 14
US-10-239-676-28/c
Sequence 28, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 28
LENGTH: 17848
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (6075, 8510, 8516, 8680, 9019, 15666)
US-10-239-676-28
Query Match
Best Local Similarity 2.8%; Score 46.4; DB 14; Length 17848;
Best Local Similarity 45.6%; Pred. No. 8.7; Mismatches 164; Indels 0; Gaps 0;
Matches 164; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 1088 AGCTTTTCCTAAATTTAAAGTAAATCTTTTTCGCTAACCAATTAATATTGAA 1147
 Db 10047 AACTTAAAAAACAATTTTAAAAATTTAAAAATTAACCACTAATTAAATTAATTC 9988
 QY 1148 ATCTTCCACCATGAAAGTTAAATTTGATCAGGATGGAAATTTGTCAAAAGCTA 1207
 Db 9987 AAAAAATATAAAATTAATAAAATTAATTAATACTAAAAATTTTAAAAAATAAAATC 9928
 QY 1208 GGTATTTCACTTTGGAGTGTACTAGTACTAGTAAGTACTAACCGAATGAGTTGTGAT 1267
 Db 9927 ATAAATATATACTAAAAATTTAAAAAATAATTAATTAATTAACATTTTAAATTTCTTT 9868
 QY 1268 TTTCGATTTTGAAGTTTCTTAGCTAAAAACAATATATTACTTAAACAATAAAGAA 1327
 Db 9867 TATAAAAAAATTTAAACAATATTTTAAATTAACAAAAATAATCTTAATTAATAAAAAA 9808
 QY 1328 AAACATTTTGTGAANAAGAAATAAGTTTACTGTGACCCCATGTACAGATGTCCTCA 1387
 Db 9807 AATTAAATTAATCGAAACAAAAAATAAATTAATTAATAATTTTAAACAAAAAATA 9748
 1388 ATAAATACGATAGAAAGATTAAGCAATGAAAGTGAATTTGTTCACTGTGTACATCGAAT 1447
 Db 9747 AAATCTATATACCAATAAAAATAATTAATTAATCTTAATAAAAAACAATTAATCTCCTAAT 9688

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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 12:00:51 ; Search time 210.848 Seconds
(without alignments)
8311.439 Million cell updates/sec

Title: US-09-938-842A-1034

Perfect score: 1071

Sequence: 1 atgagcgaacatcgaagct.....cagcgatcgcgaaccactga 1071

Scoring table: OLIGO-NUC
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

W size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	1.9	78810	US-09-949-016-16198	Sequence 16198, A
2	1.8	2556	US-09-489-039A-6112	Sequence 6112, Ap
3	1.8	34094	US-09-292-034-1	Sequence 1, Appl
4	1.8	168394	US-09-949-016-13002	Sequence 13002, A
5	1.7	372	US-09-902-540-5948	Sequence 5948, Ap
6	1.7	1527	US-09-489-039A-716	Sequence 716, App
7	1.7	1720	US-09-902-540-198	Sequence 198, Appl
8	1.7	4261	US-09-976-594-3	Sequence 16873, A
9	1.7	35688	US-09-949-016-16873	Sequence 12101, A
10	1.7	94879	US-09-949-016-12101	Sequence 13393, A
11	1.7	94884	US-09-949-016-13393	Sequence 1, Appl
12	1.7	162450	US-09-345-882-1	Sequence 14033, A
13	1.7	784019	US-09-949-016-14033	Sequence 12777, A
14	1.7	828152	US-09-949-016-12777	Sequence 1, Appl
15	1.7	1664976	US-08-916-4218-1	Sequence 24082, A
16	1.7	1664976	US-09-692-570-1	Sequence 1834, Ap
17	1.6	318	US-09-513-999C-24082	Sequence 12761, A
18	1.6	338	US-09-640-211A-1834	Sequence 186, App
19	1.6	396	US-09-248-796A-12761	Sequence 454, App
20	1.6	447	US-09-328-352-186	Sequence 15736, A
21	1.6	494	US-09-270-767-454	Sequence 2, Appl
22	1.6	494	US-08-510-878-2	Sequence 178644, A
23	1.6	516	US-09-949-016-178644	Sequence 178645, A
24	1.6	601	US-09-949-016-178645	Sequence 178646, A
25	1.6	601	US-09-949-016-178646	Sequence 184362, A
26	1.6	601	US-09-949-016-184362	
27	1.6	601	US-09-949-016-184362	

28	1.6	601	US-09-949-016-184363	Sequence 184363, A
29	1.6	675	US-09-640-211A-459	Sequence 459, App
30	1.6	748	US-08-510-878-3	Sequence 3, Appl
31	1.6	779	US-09-270-767-13769	Sequence 13769, A
32	1.6	864	US-09-976-594-1054	Sequence 1054, App
33	1.6	864	US-09-919-039-385	Sequence 385, App
34	1.6	867	US-09-252-991A-6878	Sequence 6878, Ap
35	1.6	882	US-09-252-991A-6792	Sequence 6792, Ap
36	1.6	900	US-09-050-739-59	Sequence 59, Appl
37	1.6	1251	US-09-614-912-81	Sequence 81, Appl
38	1.6	1290	US-09-902-540-9103	Sequence 9103, Ap
39	1.6	1353	US-08-611-280-1	Sequence 1, Appl
40	1.6	1353	US-09-195-940-1	Sequence 1, Appl
41	1.6	1353	US-09-562-466-1	Sequence 6792, Ap
42	1.6	1636	US-09-614-912-69	Sequence 69, Appl
43	1.6	1758	US-09-489-039A-3108	Sequence 3108, Ap
44	1.6	1960	US-09-553-867A-42	Sequence 42, Appl
45	1.6	3758	US-08-323-477-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-16198
Sequence 16198, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16198
LENGTH: 78810
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(78810)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16198
Query Match 1.9%; Score 20; DB 4; Length 78810;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1029 CCACTTCATGACACACCA 1048
DB 17829 CCACTTCATGACACACCA 17848
RESULT 2
US-09-489-039A-6112
Sequence 6112, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6112
LENGTH: 2556
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6112

Query Match
Best Local Similarity 1.8%; Score 19; DB 4; Length 2556;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 AGCTCCAGCGCTTCGACA 198
Db 850 AGCTCCAGCGCTTCGACA 868

RESULT 3

US-09-292-034-1
Sequence 1, Application US/09292034
Patent No. 6492343
GENERAL INFORMATION:

APPLICANT: Reddy, P. Seshidhar
APPLICANT: Tikoo, Suresh
APPLICANT: Bablu, Lorne
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
FILE REFERENCE: 293102002400
CURRENT APPLICATION NUMBER: US/09/292,034
CURRENT FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 34094
TYPE: DNA
ORGANISM: Porcine Adenovirus Type 3
FEATURE:
US-09-292-034-1

Query Match
Best Local Similarity 1.8%; Score 19; DB 4; Length 34094;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 850 AGCAGCGGCTTGTTCG 868
Db 21527 AGCAGCGGCTTGTTCG 21545

RESULT 4

US-09-949-016-13002/C
Sequence 13002, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13002
LENGTH: 168394
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(168394)

OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13002

Query Match
Best Local Similarity 1.8%; Score 19; DB 4; Length 168394;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 545 TTTCAGCTTCTCCGGTTT 563
Db 77366 TTTCAGCTTCTCCGGTTT 77348

RESULT 5

US-09-902-540-5948
Sequence 5948, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 5948
LENGTH: 372
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-5948

Query Match
Best Local Similarity 1.7%; Score 18; DB 4; Length 372;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 GCCGATGATGCGTCGTT 167
Db 234 GCCGATGATGCGTCGTT 251

RESULT 6

US-09-489-039A-716
Sequence 716, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 716
LENGTH: 1527
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-716

Query Match
Best Local Similarity 1.7%; Score 18; DB 4; Length 1527;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 AGCGGAGCGCGTATGC 160
Db 965 AGCGGAGCGCGTATGC 982

RESULT 7

US-09-902-540-198
; Sequence 198, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Miegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(13849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 198
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-198

Query Match 1.7%; Score 18; DB 4; Length 1720;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 GCCGGTATGCCGCTGTT 167
Db 234 GCCGGTATGCCGCTGTT 251

RESULT 8
US-09-976-594-3/C
; Sequence 3, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 4261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6673549 1863336CBI
; US-09-976-594-3

Query Match 1.7%; Score 18; DB 4; Length 4261;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 603 AGCTCTGCATCATCCAC 620
Db 3322 AGCTCTGCATCATCCAC 3305

RESULT 9
US-09-949-016-16873/C
; Sequence 16873, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16873
; LENGTH: 35688
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16873

Query Match 1.7%; Score 18; DB 4; Length 35688;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 473 TGGGTGAATCTGATGA 490
Db 30454 TGGGTGAATCTGATGA 30437

RESULT 10
US-09-949-016-12101/C
; Sequence 12101, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12101
; LENGTH: 94879
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1) -(94879)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-12101

Query Match 1.7%; Score 18; DB 4; Length 94879;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 510 TTCTAAGTGTGATATAT 527
Db 76650 TTCTAAGTGTGATATAT 76633

RESULT 11
US-09-949-016-13393/C
; Sequence 13393, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 13393
LENGTH: 94884
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) - (94884)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13393

Query Match 1.7%; Score 18; DB 4; Length 94884;
Local Similarity 100.0%; Pred. No. 46;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 510 TTCTACGCGAGTATAT 527
DB 76650 TTCTACGCGAGTATAT 76633

RESULT 12
US-09-345-882-1
Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougenetec, Lydie
TITLE OR INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pn
SEQ ID NO: 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:

NAME/KEY: allele
LOCATION: 99098
OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
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NAME/KEY: allele
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FEATURE:
NAME/KEY: allele
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NAME/KEY: allele
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NAME/KEY: allele
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OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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NAME/KEY: allele


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LOCATION: 88050..88096
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NAME/KEY: allele
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NAME/KEY: allele
LOCATION: 108084..108130

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 35413 TCGAGAGCTTCTCTTGA 35430
RESULT 13
US-09-949-016-14033/C
Sequence 14033, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14033
LENGTH: 784019
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(784019)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033
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Db 136173 CTGAGAGCTTCTCCCTA 136156
RESULT 14
US-09-949-016-12777/C
Sequence 12777, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

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;; PRIOR FILING DATE: 2000-09-08
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;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 12777
;; LENGTH: 828152
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
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;;   LOCATION: (1)...(828152)
;;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

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Best Local Similarity 100.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
; Patent No. 6503729
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
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SEQ ID NO 1
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/ US-08-916-421B-1
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Best Local Similarity 100.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
QY 170 CAATGCTTTAGCTCAG 187
DB 1522815 CAATGCTTTAGCTCAG 1522798
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Search completed: February 28, 2005, 16:17:21
Job time : 218.848 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 08:18:05 ; Search time 673.467 Seconds
(without alignments)
9423.127 Million cell updates/sec

Title: US-09-938-842A-1034

Perfect score: 1071

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Gapop 60.0 , Gapext 60.0

Searched: 5394803 seqs, 2962729879 residues

W size: 0

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1071	100.0	1071	9	US-09-938-842A-1034
2	1071	100.0	1071	11	US-09-938-842A-1034
3	289	27.0	460	9	US-09-924-035A-502
4	286	26.7	453	9	US-09-770-444-615
5	185	17.3	185	9	US-09-770-696-257
6	25	2.3	704	17	US-10-225-066A-1049
7	25	2.3	704	17	US-10-374-780A-2683
8	23	2.1	390	11	US-09-732-627A-4287
9	23	2.1	587	18	US-10-021-323-15482
10	23	2.1	938	18	US-10-767-795-3984
11	23	2.1	1604	15	US-10-295-403-147

12	23	2.1	1604	17	US-10-412-699B-551	Sequence 551, App
13	21	2.0	755	18	US-10-363-345A-33693	Sequence 33693, A
14	21	2.0	755	18	US-10-363-345A-33694	Sequence 33694, A
15	20	1.9	432	18	US-10-425-115-164143	Sequence 164143, A
16	20	1.9	442	17	US-10-424-599-59834	Sequence 59834, A
17	20	1.9	453	17	US-10-276-774-292	Sequence 292, App
18	20	1.9	1263	17	US-10-369-493-37704	Sequence 37704, A
19	20	1.9	1756	17	US-10-424-599-93501	Sequence 93501, A
20	20	1.9	94810	17	US-10-052-482-22	Sequence 22, Appl
21	20	1.9	125534	13	US-10-087-192-1678	Sequence 1678, App
22	20	1.8	343	18	US-10-425-115-73537	Sequence 73537, A
23	19	1.8	600	18	US-10-363-345A-30293	Sequence 30293, A
24	19	1.8	600	18	US-10-363-345A-30294	Sequence 30294, A
25	19	1.8	926	17	US-10-425-114-2989	Sequence 2989, App
26	19	1.8	1065	17	US-10-425-114-3219	Sequence 3219, App
27	19	1.8	1081	17	US-10-425-114-15522	Sequence 15522, A
28	19	1.8	1116	17	US-10-425-114-15510	Sequence 15510, A
29	19	1.8	1176	17	US-10-425-114-14614	Sequence 14614, A
30	19	1.8	1212	18	US-10-425-115-73538	Sequence 73538, A
31	19	1.8	1520	18	US-10-425-115-4945	Sequence 4945, App
32	19	1.8	2360	18	US-10-425-115-73545	Sequence 73545, A
33	19	1.8	2408	18	US-10-425-115-139810	Sequence 139810, A
34	19	1.8	2486	18	US-10-425-115-73540	Sequence 73540, A
35	19	1.8	2727	18	US-10-437-963-59921	Sequence 59921, A
36	19	1.8	4459	18	US-10-437-963-53427	Sequence 53427, A
37	19	1.8	34094	14	US-09-963-038A-1	Sequence 1, Appl1
38	19	1.8	34094	14	US-10-199-550-1	Sequence 1, Appl1
39	19	1.8	34094	15	US-10-245-603A-1	Sequence 1, Appl1
40	19	1.8	62647	18	US-10-332-281-274	Sequence 274, App
41	19	1.8	148815	13	US-10-087-192-1873	Sequence 1873, App
42	18	1.7	223	9	US-10-437-963-61567	Sequence 61567, A
43	18	1.7	277	9	US-09-294-093B-4716	Sequence 4716, App
44	18	1.7	317	18	US-10-767-701-18118	Sequence 18118, A
45	18	1.7	364	10	US-09-918-995-30316	Sequence 30316, A

ALIGNMENTS

RESULT 1
US-09-938-842A-1034
; Sequence 1034, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1034
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1034

Query Match 100.0%; Score 1071; DB 9; Length 1071;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	241	AAGGTTAAGAGAAAGGAGAGAGATACGATGCTCTGCAAGTGCGTGCGCTAGATATTTT	300
Db	241	AAGGTTAAGAGAAAGGAGAGAGATACGATGCTCTGCAAGTGCGTGCGCTAGATATTTT	300
QY	301	CAATTAACCTGAGAGGTTAAGTTCACAAATCCGACGGCGAAACGATTCGTTGTTTGAG	360
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QY	361	AAGCGTAGCGCGCGAATTATAGCGCGCACGGATACGGGAAACGGTTCGCGCAATCGCAG	420
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QY	601	CAGGCTCTGGCATCATCCACTGTGGCTACGAACTTCTGCGGCAAGAAATGATCCGATG	660
Db	601	CAGGCTCTGGCATCATCCACTGTGGCTACGAACTTCTGCGGCAAGAAATGATCCGATG	660
QY	661	TGGGCTAATTCATCAAAACGAAATGATTCGACGGTCCGAGCTTCTTTGATTTCCACAA	720
Db	661	TGGGCTAATTCATCAAAACGAAATGATTCGACGGTCCGAGCTTCTTTGATTTCCACAA	720
QY	721	ATCGCTGGTCCGTGCAATGAGCTTGAATTAAGCTTTTCCGCGCGCGCTGTTCCGCG	780
Db	721	ATCGCTGGTCCGTGCAATGAGCTTGAATTAAGCTTTTCCGCGCGCGCTGTTCCGCG	780
QY	781	TGCTTTAAGTCCGCGGCTTCAACAGGCTTCCACAGATGCTTAACACCTCTCTTAA	840
Db	781	TGCTTTAAGTCCGCGGCTTCAACAGGCTTCCACAGATGCTTAACACCTCTCTTAA	840
QY	841	GTTGTTCCAAACACGCGCTTGTATCCGTTTCAACGTTTACGCTTGAATTTATCAAGA	900
Db	841	GTTGTTCCAAACACGCGCTTGTATCCGTTTCAACGTTTACGCTTGAATTTATCAAGA	900
QY	901	GCGAGTTCGATTATGCTCCGAGCTCAAGCTCAAGGGCTAACACCGGTATGATCATGCTCA	960
Db	901	GCGAGTTCGATTATGCTCCGAGCTCAAGCTCAAGGGCTAACACCGGTATGATCATGCTCA	960
QY	961	ATTGCAACAACAAGACGACACGCTGAGACTTCTCCCTAGATATATCAGAAACAA	1020
Db	961	ATTGCAACAACAAGACGACACGCTGAGACTTCTCCCTAGATATATCAGAAACAA	1020
QY	1021	GAGCTTACCAAGTTCATGACACCAACAAGACGCGATACGAAACCACTGCA	1071
Db	1021	GAGCTTACCAAGTTCATGACACCAACAAGACGCGATACGAAACCACTGCA	1071

```

: PublicationNo. US20040009476A9
:
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Krepes, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SC91P300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1034
: LENGTH: 1071
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: US-09-938-842A-1034

```

Query Match	Best Local Similarity	100.0%	Score 1071	DB 11	Length 1071
Matches 1071	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
Qy	1	ATGGCGACAAATTCAGAAAGCTTGAAGAAGTTGGAGGCAAGATCAAACTCTTAAGAGCGGTT	60		
Db	1	ATGGCGACAAATTCAGAAAGCTTGAAGAAGTTGGAGGCAAGATCAAACTCTTAAGAGCGGTT	60		
Qy	61	GATCTAACCATATCATCAACGGCGTCGAAAACGTCGAAATTCGAAGCCTTTCCAAAGTAAT	120		
Db	61	GATCTAACCATATCATCAACGGCGTCGAAAACGTCGAAATTCGAAGCCTTTCCAAAGTAAT	120		
Qy	121	CCCAAGTGAAGTCTCGAGGCCAAGGCGGAGCGGTGATGCGTGGTTTTCATGTCCTTA	180		
Db	121	CCCAAGTGAAGTCTCGAGGCCAAGGCGGAGCGGTGATGCGTGGTTTTCATGTCCTTA	180		
Qy	181	GCTCCACCGTCTTTCGACGAGCCACCAATTTGAAGAAGCTTCGACTTAAGACCGTCACAG	240		
Db	181	GCTCCACCGTCTTTCGACGAGCCACCAATTTGAAGAAGCTTCGACTTAAGACCGTCACAG	240		
Qy	241	AAAGTTGAAGAAAGGAGGAGGAAGATACGATGCGTCTCCAGTGTGTGGCGCTAGAGATTTT	300		
Db	241	AAAGTTGAAGAAAGGAGGAGGAAGATACGATGCGTCTCCAGTGTGTGGCGCTAGAGATTTT	300		
Qy	301	CAATTAATCTCGAGAGTTAGGTCAAAATCCGACGCGCAAAACGATTCGGTGTGTTGGAG	360		
Db	301	CAATTAATCTCGAGAGTTAGGTCAAAATCCGACGCGCAAAACGATTCGGTGTGTTGGAG	360		
Qy	361	AAAGCTGAGCGCGGATTAATAGCCGCCACGCGGTACGGAAGCGTTCCCGCATCGCCATG	420		
Db	361	AAAGCTGAGCGCGGATTAATAGCCGCCACGCGGTACGGAAGCGTTCCCGCATCGCCATG	420		
Qy	421	TCGGTTAACGGAAACCTTAATAAATCCGACGACGACGATTCGATATGAGGTGAA	480		
Db	421	TCGGTTAACGGAAACCTTAATAAATCCGACGACGACGATTCGATATGAGGTGAA	480		
Qy	481	AATCTGATGAAGAAGAAAGCTTAACGATCTTCTAAGAGTGAATTAAGACGAAAGCGAA	540		
Db	481	AATCTGATGAAGAAGAAAGCTTAACGATCTTCTAAGAGTGAATTAAGACGAAAGCGAA	540		
Qy	541	GCCTTTACACTCTCTCCGGTTTAAAGTCCAAATTTGCCACGACGACGATCCAACTCCG	600		
Db	541	GCCTTTACACTCTCTCCGGTTTAAAGTCCAAATTTGCCACGACGACGATCCAACTCCG	600		
Qy	601	CAAGCTCTGGCATCATCACTGAGCTCAGCAACTTTCGCGCAAGAAATGATTCGAGT	660		
Db	601	CAAGCTCTGGCATCATCACTGAGCTCAGCAACTTTCGCGCAAGAAATGATTCGAGT	660		
Qy	661	TGGGCTATTTCATCAAAAGCAATGATTCGAGAGGTTCGAGACCTTTCTTTGAATTCACAA	720		

Db 661 TGGGCTATTCATCAACGCAATGATTCGACGGTCGAGCTTCTTGTGATTCACAA 720
Qy 721 ATCGTGGTCCGTCGAATCAGCTTATTAAGTTTCCCGCGCGCTCTCGCCG 780
Db 721 ATCGTGGTCCGTCGAATCAGCTTATTAAGTTTCCCGCGCGCTCTCGCCG 780
Qy 781 TCGTCTTACGTCGCGCTGTTCAACAGGCTTCCAGATGGCTAGACCACTCTTACAA 840
Db 781 TCGTCTTACGTCGCGCTGTTCAACAGGCTTCCAGATGGCTAGACCACTCTTACAA 840
Qy 841 GTTGTTCACAGCAGCGCTTGTATCCGTTTCAGACGTTAGCGGTTGCAATTTACAA 900
Db 841 GTTGTTCACAGCAGCGCTTGTATCCGTTTCAGACGTTAGCGGTTGCAATTTACAA 900
Qy 901 GCGAGCTGGTTATGCTTCGAGCTCAAGCTCAGGCTGTAACACCGGTAGTTATCTGCA 960
Db 901 GCGAGCTGGTTATGCTTCGAGCTCAAGCTCAGGCTGTAACACCGGTAGTTATCTGCA 960
Qy 961 ATTGCAACAACAAGCAGCAGCGTGAAGAGCTTCTCCCTAGATATTAAGAAACAA 1020
Db 961 ATTGCAACAACAAGCAGCAGCGTGAAGAGCTTCTCCCTAGATATTAAGAAACAA 1020
Qy 1021 GAGCTTCAACAATTGATGAGCACAACAAGCAGGCTATCGAACCACTGA 1071
Db 1021 GAGCTTCAACAATTGATGAGCACAACAAGCAGGCTATCGAACCACTGA 1071

RESULT 3

US-09-924-035A-502/C
Sequence 502, Application US/09924035A
Patent No. US20020142319A1
GENERAL INFORMATION:
APPLICANT: Grlach, Jrm
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,784
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 502
LENGTH: 460
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)_(460)
OTHER INFORMATION: n = A,T,C or G
US-09-924-035A-502

Query Match 27.0%; Score 289; DB 9; Length 460;

Best Local Similarity 99.6%; Pred. No. 1.5e-148;

Matches 459; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 600 GCAAGCTCTGGCATATCATCTGTCGCTCAGCACTTCTGCCGCAAGATATTCAGT 659
Db 460 GCAAGCTCTGGCATATCATCTGTCGCTCAGCACTTCTGCCGCAAGATATTCAGT 401
Qy 660 GTGGGCTATTCATCAACGCAATGATTCGAGCGGTCCGAGCTTCTTGTATTCACA 719
Db 400 GTGGGCTATTCATCAACGCAATGATTCGAGCGGTCCGAGCTTCTTGTATTCACA 341
Qy 720 AATCGCTGGTCCGTCGAATCAGCTTATTAAGTTTCCCGCGCGCTCTCGCC 779
Db 340 AATCGCTGGTCCGTCGAATCAGCTTATTAAGTTTCCCGCGCGCTCTCGCC 282
Qy 780 GTGCTTACGTCGCGCTGTTCAACAGGCTTCCAGATGGCTAGACCACTCTTACAA 839
Db 281 GTGCTTACGTCGCGCTGTTCAACAGGCTTCCAGATGGCTAGACCACTCTTACAA 222

Qy 840 AGTTGTCCAAGCAGCGCTTGTATCCGTTTCAGACGTTAGCGGTTGAAATTAACAAG 899
Db 221 AGTTGTCCAAGCAGCGCTTGTATCCGTTTCAGACGTTAGCGGTTGAAATTAACAAG 162
Qy 900 AGCAGCTGGTTATGCTTCGAGCTCAAGCTCAGGCTTAACACCGGTAGTTATCTGTC 959
Db 161 AGCAGCTGGTTATGCTTCGAGCTCAAGCTCAGGCTTAACACCGGTAGTTATCTGTC 102
Qy 960 AATTGCAACAACAAGCAGCAGCGTGAAGAGCTTCTCCCTAGATATTAAGAAACAA 1019
Db 101 AATTGCAACAACAAGCAGCAGCGTGAAGAGCTTCTCCCTAGATATTAAGAAACAA 42
Qy 1020 AGAGCTTCAACAATTGATGAGCACAACAAGCAGGCTATCGAACCACTGA 1060
Db 41 AGAGCTTCAACAATTGATGAGCACAACAAGCAGGCTATCGAACCACTGA 1

RESULT 4

US-09-770-444-615/C
Sequence 615, Application US/09770444
Patent No. US20020023280A1
GENERAL INFORMATION:
APPLICANT: Grlach, Jrm
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moesner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hutban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 615
LENGTH: 453
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(453)
OTHER INFORMATION: n = A,T,C or G
US-09-770-444-615

Query Match 26.7%; Score 286; DB 9; Length 453;

Best Local Similarity 100.0%; Pred. No. 6.8e-147;

Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 775 TCGCGTGTCTTACGTCGCGCTGTTCAACAGGCTTCCAGATGGCTAGACCACTCTCT 834
Db 286 TCGCGTGTCTTACGTCGCGCTGTTCAACAGGCTTCCAGATGGCTAGACCACTCTCT 227
Qy 835 TTACAAGTTGTTCAAGCAGCGCTTGTATCCGTTTCAGACGTTAGGCTTCAATTAA 894
Db 226 TTACAAGTTGTTCAAGCAGCGCTTGTATCCGTTTCAGACGTTAGGCTTCAATTAA 167
Qy 895 TCAAGAGCAGCTGGTTATGCTCCAGCTCAAGCTCAGGCTGAACACCGGTAGTTCA 954

Db 166 TCAGAGGACGCTGGTATGCTCCGAGCTCAAGCTCAGCGTAAACACCGGTAGTTCA 107
Qy 955 TCGTCAATTTGCAACAACAGACGACACGCTGAGAGACTTCTCCCTAGAGATATACGAG 1014
Db 106 TCGTCAATTTGCAACAACAGACGACACGCTGAGAGACTTCTCCCTAGAGATATACGAG 47
Qy 1015 AAACAAGAGCTTCCAGCTTCATGAGCACCACCAACAGCAGCTCAT 1060
Db 46 AAACAAGAGCTTCCAGCTTCATGAGCACCACCAACAGCAGCTCAT 1

RESULT 5
US-09-770-696-257
Sequence 257, Application US/09770696
Patent No. US2001004940A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moesner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Huban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2031US (PAPA-020PRV)
CURRENT APPLICATION NUMBER: US/09/770,696
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,278
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 257
LENGTH: 185
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-770-696-257

Query Match 17.3%; Score 185; DB 9; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.3e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 35 GCAAGATCAACCTTAAGCCGCTGATTAACCTCAATCAACGCGCTCAGAAAAGCTCG 94
Db 1 GCAAGATCAACCTTAAGCCGCTGATTAACCTCAATCAACGCGCTCAGAAAAGCTCG 60
Qy 95 AAATTCAGACCTTTCCAGTAAATCCACAGTAGTCTCCAGGCCCAAGGGCGGAGCGG 154
Db 61 AAATTCAGACCTTTCCAGTAAATCCACAGTAGTCTCCAGGCCCAAGGGCGGAGCGG 120
Qy 155 TGATGCCGCTGTTTAAATCTCTTAAAGCTCCACCGCTTTCAGACAGACCATTTGAGA 214
Db 121 TGATGCCGCTGTTTAAATCTCTTAAAGCTCCACCGCTTTCAGACAGACCATTTGAGA 180
Qy 215 GAGCT 219
Db 181 GAGCT 185

RESULT 6

US-10-225-066A-1049
Sequence 1049, Application US/10225066A
Publication No. US2003026173A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBEL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: PILGRIM, Marsha L
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lynne
APPLICANT: CREELMAN, Robert A
APPLICANT: PINEDA, Omaira
APPLICANT: YU, Guo-Liang
APPLICANT: BROUN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1049
LENGTH: 704
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-225-066A-1049

Query Match 2.3%; Score 25; DB 17; Length 704;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 222 GACTTAAGACCGTCACACGAGGTT 246
Db 189 GACTTAAGACCGTCACACGAGGTT 213

RESULT 7
US-10-374-780A-2689
Sequence 2689, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddle, James
APPLICANT: Broun, Pierre E
APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MB1-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944

PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
ID NO: 2689
LENGTH: 704
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1663
US-10-374-780A-2689

Query Match 2.3%; Score 25; DB 17; Length 704;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GACTAAGACCGTCACGAGAGTT 246
DB 189 GACTAAGACCGTCACGAGAGTT 213

RESULT 8
US-09-732-627A-4287
Sequence 4287, Application US/09732627A
Publication No. US20040123338A1
GENERAL INFORMATION:
APPLICANT: Fincher, Karen L.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(51770)B
CURRENT APPLICATION NUMBER: US/09/732,627A
CURRENT FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 4930
ID NO: 4287
LENGTH: 390
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3493-028-P1-M1-F9
US-09-732-627A-4287

Query Match 2.1%; Score 23; DB 11; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 ACTAAGACCGTCACGAGAGT 245
DB 43 ACTAAGACCGTCACGAGAGT 65

RESULT 9
US-10-021-323-15482
Sequence 15482, Application US/100212323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, J111
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.

APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
ID NO: 15482
LENGTH: 587
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3829-026-Q6-K6-G6
US-10-021-323-15482

Query Match 2.1%; Score 23; DB 18; Length 587;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 ACTAAGACCGTCACGAGAGT 245
DB 257 ACTAAGACCGTCACGAGAGT 279

RESULT 10
US-10-767-795-3984
Sequence 3984, Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
ID NO: 3984
LENGTH: 938
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
OTHER INFORMATION: Clone ID: GOSH-09MAY01-C3741_1
US-10-767-795-3984

Query Match 2.1%; Score 23; DB 18; Length 938;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 ACTAAGACCGTCACGAGAGT 245
DB 258 ACTAAGACCGTCACGAGAGT 280

RESULT 11
US-10-295-403-147
Sequence 147, Application US/10295403
Publication No. US20030101481A1
GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Riechmann, Jose Luis
APPLICANT: Adam, Luc
APPLICANT: Brown, Pierre
APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddle, James
APPLICANT: Zhang, James
APPLICANT: Benito, Maria-Ines
APPLICANT: Yu, Guo-Liang


```
APPLICANT: Fromm, Mike
; TITLE OF INVENTION: PLANT GENE SEQUENCES I
; FILE REFERENCE: MBI-0003
; CURRENT APPLICATION NUMBER: US/10/295,403
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/101,349
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/103,312
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/108,734
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/113,409
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 147
; LENGTH: 1604
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (143)..(1345)
; OTHER INFORMATION: G802
US-10-295-403-147

Query Match
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 TCGACTTAAAGACCGTCACACGAA 242
Db 317 TCGACTTAAAGACCGTCACACGAA 339

RESULT 12
US-10-412-699B-551
; Sequence 551, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Brineda, Omaria
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgrim, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kumimoto, Bradley K.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
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; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 551
; LENGTH: 1604
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G802
US-10-412-699B-551
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 TCGACTTAAAGACCGTCACACGAA 242
Db 317 TCGACTTAAAGACCGTCACACGAA 339
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RESULT 13
US-10-363-345A-33693/C
; Sequence 33693, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33693
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-33693
```

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Query Match
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 AAAAATCCCGACGACGACGAA 458
Db 88 AAAAATCCCGACGACGACGAA 68
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RESULT 14
US-10-363-345A-33694
; Sequence 33694, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: cytosines in genomic DNA in the sequence context of 5'-CpG-3
```



```

; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33694
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-33694

```

```

Query Match          2.0%; Score 21; DB 18; Length 755;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 438 AAAAATCCGACGACGACGAA 458
DB 668 AAAAATCCGACGACGACGAA 688

```

```

RESULT 15
US-10-425-115-164143/C
; Sequence 164143, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: LA ROBA, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 164143
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_81277C.1
US-10-425-115-164143

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```

Query Match          1.9%; Score 20; DB 18; Length 432;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 767 CCGCTGCTTCGCGCTGCT 786
DB 289 CCGCTGCTTCGCGCTGCT 270

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Search completed: February 28, 2005, 12:54:07
 Job time : 675.967 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 12:00:51 / Search time 330.152 Seconds
(without alignments)
8311.439 Million cell updates/sec

Title: US-09-938-842a-3729

Perfect score: 1677

Sequence: 1 ggttaagcgttactatg.....ttcttcacgtatattta 1677

Scoring table: OLIGO-MUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued Patents, NA:*

1: /cgn2_6/pdata/1/ina/5A_COMB.seq:*
2: /cgn2_6/pdata/1/ina/5B_COMB.seq:*
3: /cgn2_6/pdata/1/ina/RA_COMB.seq:*
4: /cgn2_6/pdata/1/ina/5B_COMB.seq:*
5: /cgn2_6/pdata/1/ina/5B_COMB.seq:*
6: /cgn2_6/pdata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	1.1	400	US-08-956-171E-3898	Sequence 3898, Ap
2	19	1.1	400	US-08-781-986A-3898	Sequence 3898, Ap
3	19	1.1	601	US-09-949-016-23701	Sequence 23701, A
4	19	1.1	601	US-09-949-016-163444	Sequence 163444, A
5	19	1.1	7563	US-08-956-171E-33	Sequence 33, Appl
6	19	1.1	7563	US-08-781-986A-33	Sequence 33, Appl
7	19	1.1	85869	US-09-949-016-12017	Sequence 12017, A
8	19	1.1	85878	US-09-949-016-16321	Sequence 16321, A
9	19	1.1	90724	US-09-949-016-16601	Sequence 16601, A
10	19	1.1	94095	US-09-949-016-14389	Sequence 14389, A
11	19	1.1	177293	US-09-949-016-16513	Sequence 16513, A
12	19	1.1	321022	US-09-949-016-11852	Sequence 11852, A
13	19	1.1	321022	US-10-121-857-58	Sequence 58, Appl
14	19	1.1	342	US-09-270-767-3134	Sequence 3134, Ap
15	18	1.1	493	US-09-270-767-18416	Sequence 18416, A
16	18	1.1	601	US-09-949-016-136404	Sequence 136404, A
17	18	1.1	601	US-09-949-016-136405	Sequence 136405, A
18	18	1.1	601	US-09-949-016-136405	Sequence 136405, A
19	18	1.1	832	US-08-340-539A-6	Sequence 6, Appl
20	18	1.1	832	US-08-461-592B-6	Sequence 6, Appl
21	18	1.1	876	US-09-198-119C-48	Sequence 48, Appl
22	18	1.1	876	US-09-601-802D-48	Sequence 48, Appl
23	18	1.1	877	US-09-198-119C-72	Sequence 72, Appl
24	18	1.1	877	US-09-601-802D-72	Sequence 72, Appl
25	18	1.1	887	US-09-198-119C-68	Sequence 68, Appl
26	18	1.1	887	US-09-601-802D-68	Sequence 68, Appl
27	18	1.1	887	US-09-601-802D-68	Sequence 68, Appl

C 28	18	1.1	949	US-09-270-767-25118	Sequence 25118, A
C 29	18	1.1	1028	US-09-249-180-1	Sequence 1, Appl
C 30	18	1.1	1132	US-09-198-119C-56	Sequence 56, Appl
C 31	18	1.1	1132	US-09-601-802D-56	Sequence 56, Appl
C 32	18	1.1	1163	US-09-249-180-5	Sequence 5, Appl
C 33	18	1.1	1185	US-09-134-000C-927	Sequence 927, Appl
C 34	18	1.1	1235	US-09-270-767-9828	Sequence 9828, Ap
C 35	18	1.1	1380	US-09-543-681A-2115	Sequence 2115, Ap
C 36	18	1.1	1496	US-09-895-652A-2	Sequence 2, Appl
C 37	18	1.1	2048	US-09-328-352-2704	Sequence 2704, Ap
C 38	18	1.1	5070	US-09-853-450-44	Sequence 44, Appl
C 39	18	1.1	18031	US-09-902-540-1180	Sequence 1180, Ap
C 40	18	1.1	22914	US-09-949-016-12489	Sequence 12489, A
C 41	18	1.1	22914	US-09-949-016-15613	Sequence 15613, A
C 42	18	1.1	26711	US-09-949-016-14214	Sequence 14214, A
C 43	18	1.1	32104	US-09-949-016-14722	Sequence 14722, A
C 44	18	1.1	53789	US-09-949-016-12137	Sequence 12137, A
C 45	18	1.1	53789	US-09-949-016-13955	Sequence 13955, A

ALIGNMENTS

RESULT 1

US-08-956-171E-3898/C

Sequence 3898, Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunach

Gill H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Farnon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 3898:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

US-08-956-171E-3898

Query Match 1.1%; Score 19; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 TTGTTGAATGCTTTTCA 67
Db 129 TTGTTGAATGCTTTTCA 111

RESULT 2

US-08-781-986A-3898/C
Sequence 3898, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PR248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 3898:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-3898

Query Match 1.1%; Score 19; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 TTGTTGAATGCTTTTCA 67
Db 129 TTGTTGAATGCTTTTCA 111

RESULT 3

US-09-949-016-23701/C
Sequence 23701, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23701
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-23701

Query Match 1.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1317 CAATPAAAGAAAACATTT 1335
Db 43 CAATPAAAGAAAACATTT 25

RESULT 4

US-09-949-016-163444/C
Sequence 163444, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 163444
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-163444

Query Match 1.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1317 CAATPAAAGAAAACATTT 1335
Db 43 CAATPAAAGAAAACATTT 25

RESULT 5

US-08-956-171B-33/C
Sequence 33, Application US/08956171B
Patent No. 6593114

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland

COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 7563 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-956-171E-33

Query Match 1.1%; Score 19; DB 4; Length 7563;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 49 TTGTTGAATGCTTTTCA 67
Db 2292 TTGTTGAATGCTTTTCA 2274

RESULT 6
US-08-781-986A-33/c
Sequence 33, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 7563 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-33

Query Match 1.1%; Score 19; DB 4; Length 7563;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 49 TTGTTGAATGCTTTTCA 67
Db 2292 TTGTTGAATGCTTTTCA 2274

RESULT 7
US-09-949-016-12017
Sequence 12017, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12017
LENGTH: 85869
TYPE: DNA
ORGANISM: Human
US-09-949-016-12017

Query Match 1.1%; Score 19; DB 4; Length 85869;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1317 CATATAAGAAAACATTT 1335
Db 65772 CATATAAGAAAACATTT 65790

RESULT 8
US-09-949-016-16321
Sequence 16321, Application US/09949016
Patent No. 6812338
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16321

LENGTH: 85878
TYPE: DNA
ORGANISM: Human
US-09-949-016-16321

Query Match
Best Local Similarity 1.1%; Score 19; DB 4; Length 85878;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1317 CATTAAGAAAACATT 1335
DB 65772 CATTAAGAAAACATT 65790

RESULT 9
US-09-949-016-16601

Sequence 16601, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C0001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16601

LENGTH: 90724

TYPE: DNA

ORGANISM: Human

US-09-949-016-16601

Query Match
Best Local Similarity 1.1%; Score 19; DB 4; Length 90724;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1259 GTTCGATTGATTTT 1277
DB 42588 GTTCGATTGATTTT 42606

RESULT 10
US-09-949-016-14389/c

Sequence 14389, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C0001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14389

LENGTH: 94095

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(94095)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14389

Query Match
Best Local Similarity 1.1%; Score 19; DB 4; Length 94095;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AATGCTTCAGGCTTTGT 118
DB 68048 AATGCTTCAGGCTTTGT 68030

RESULT 11
US-09-949-016-16513

Sequence 16513, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C0001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16513

LENGTH: 177293

TYPE: DNA

ORGANISM: Human

US-09-949-016-16513

Query Match
Best Local Similarity 1.1%; Score 19; DB 4; Length 177293;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 TTTTCATTAATTTAAAGT 1110
DB 117431 TTTTCATTAATTTAAAGT 117449

RESULT 12
US-09-949-016-11852

Sequence 11852, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C0001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11852

LENGTH: 321022

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(321022)

OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11852

Query Match 1.1%; Score 19; DB 4; Length 321022;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TGCTTTTCAGATCATCAA 76
DB 283681 TGCTTTTCAGATCATCAA 283699

RESULT 13

US-09-949-016-14166
Sequence 14166, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14166
LENGTH: 321022
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(321022)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14166

Query Match 1.1%; Score 19; DB 4; Length 321022;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TGCTTTTCAGATCATCAA 76
DB 283681 TGCTTTTCAGATCATCAA 283699

RESULT 14

US-10-121-857-58
Sequence 58, Application US/10121857
Patent No. 6822141
GENERAL INFORMATION:
APPLICANT: Lardizabal, Kathryn D
APPLICANT: Hawkins, Deborah J
APPLICANT: Thompson, Gregory A
TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
FILE REFERENCE: 16515.143
CURRENT APPLICATION NUMBER: US/10/121,857
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 09/345,461
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,631
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: US 60/130,829
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 342
TYPE: DNA

ORGANISM: murine
US-10-121-857-58

Query Match 1.1%; Score 18; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1186 TGAATTTTGTACCAA 1203
DB 267 TGAATTTTGTACCAA 284

RESULT 15

US-09-270-767-3134
Sequence 3134, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3134
LENGTH: 493
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-3134

Query Match 1.1%; Score 18; DB 4; Length 493;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1104 TTAAGTAATCTTTT 1121
DB 363 TTAAGTAATCTTTT 380

Search completed: February 28, 2005, 16:17:24
Job time : 333.152 secs

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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 08:18:05 ; Search time 1054.53 Seconds
(without alignment)

9423.127 Million cell updates/sec

Title: US-09-938-842a-3729

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Gapop 60.0 , Gapext 60.0

Searched: 5394803 seqs, 2962729879 residues

Size: 0

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1677	100.0	1677	US-09-938-842a-3729	Sequence 3729, Ap
3	23	1.4	174448	US-10-087-192-148	Sequence 148, App
4	21	1.3	330	US-09-930-213-54	Sequence 54, Appl
5	21	1.3	394	US-09-803-719-707	Sequence 707, App
6	21	1.3	406	US-10-424-599-103891	Sequence 103891, App
7	21	1.3	407	US-09-803-719-1633	Sequence 1633, Ap
8	21	1.3	2000	US-09-930-213-306	Sequence 306, App
9	21	1.3	108359	US-10-191-807-3	Sequence 3, Appl
10	21	1.3	133462	US-10-367-094-114	Sequence 114, App
11	20	1.2	627	US-10-027-632-54726	Sequence 54726, A

C 12	20	1.2	627	13	US-10-027-632-294129	Sequence 294129, A
C 13	20	1.2	627	17	US-10-027-632-54726	Sequence 54726, A
C 14	20	1.2	627	17	US-10-027-632-284129	Sequence 284129, A
C 15	20	1.2	628	18	US-10-437-963-9063	Sequence 9063, Ap
C 16	20	1.2	768	9	US-09-815-242-9987	Sequence 9987, Ap
C 17	20	1.2	768	17	US-10-282-122A-39631	Sequence 39631, A
C 18	20	1.2	769	17	US-10-282-122A-36869	Sequence 36869, A
C 19	20	1.2	1793	17	US-10-424-599-63060	Sequence 63060, A
C 20	20	1.2	6059	18	US-10-437-963-10677	Sequence 10677, A
C 21	20	1.2	6499	18	US-10-437-963-101721	Sequence 101721, A
C 22	19	1.1	199	16	US-10-029-386-14103	Sequence 14103, A
C 23	19	1.1	281	17	US-10-242-5535A-18166	Sequence 18166, A
C 24	19	1.1	281	17	US-10-085-7633A-18166	Sequence 18166, A
C 25	19	1.1	307	18	US-10-437-963-36666	Sequence 36666, A
C 26	19	1.1	377	9	US-09-983-965-5678	Sequence 5678, Ap
C 27	19	1.1	400	8	US-08-781-986A-3898	Sequence 3898, Ap
C 28	19	1.1	400	17	US-10-329-624-3898	Sequence 3898, Ap
C 29	19	1.1	502	18	US-10-437-963-55251	Sequence 55251, A
C 30	19	1.1	547	16	US-10-029-386-398	Sequence 398, App
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C 32	19	1.1	588	13	US-10-027-632-88863	Sequence 88863, A
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C 34	19	1.1	588	17	US-10-027-632-88863	Sequence 88863, A
C 35	19	1.1	598	13	US-10-027-632-230239	Sequence 230239, A
C 36	19	1.1	598	13	US-10-027-632-230240	Sequence 230240, A
C 37	19	1.1	598	17	US-10-027-632-230239	Sequence 230239, A
C 38	19	1.1	598	17	US-10-027-632-230240	Sequence 230240, A
C 39	19	1.1	652	13	US-10-027-632-133067	Sequence 133067, A
C 40	19	1.1	652	17	US-10-027-632-133067	Sequence 133067, A
C 41	19	1.1	672	13	US-10-027-632-34038	Sequence 34038, A
C 42	19	1.1	752	18	US-10-027-632-34038	Sequence 34038, A
C 43	19	1.1	753	18	US-10-425-115-101619	Sequence 101619, A
C 44	19	1.1	903	9	US-09-815-242-2975	Sequence 2975, Ap
C 45	19	1.1	903	17	US-10-282-122A-5549	Sequence 5549, Ap

ALIGNMENTS

RESULT 1
US-09-938-842a-3729
Sequence 3729, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krepes, Joel
APPLICANT: Zhu, Tong
APPLICANT: Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPT100-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3729
LENGTH: 1677
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842a-3729

Query Match 100.0% Score 1677; DB 9; Length 1677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGTAAAGCCTTTACTTATGTTATATGCAACGAGATATATGCGATGTTGGAATCC 60


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QY 121 GAAATGTGTATTTCGAAACAGGTAGAGAAACATACCATAGACAGATGTATCTGAAGAGA 180
DB 121 GAAATGTGTATTTCGAAACAGGTAGAGAAACATACCATAGACAGATGTATCTGAAGAGA 180
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QY 241 TAAATGTTTGTAAAGAAATCTACTTATTTATGTGAATTTGTGTAGTGAAGAAAGT 300
DB 241 TAAATGTTTGTAAAGAAATCTACTTATTTATGTGAATTTGTGTAGTGAAGAAAGT 300
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DB 301 AAAAATCATGGAATCCAAACCTCAAAATTTACCAATCAGCCCAATTTATGTGTGCG 360
QY 361 TAAATGATGTATGTCTGAATGTAGGCAAAAGTTGGTGCTGCAAAATTAACAATATC 420
DB 361 TAAATGATGTATGTCTGAATGTAGGCAAAAGTTGGTGCTGCAAAATTAACAATATC 420
QY 421 CCTGTGTGTGGAACCCGAATCTGTATCGAAAAGGTGAAACCACTTGTGTAACTTTT 480
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QY 661 AGAGTAGGGTCCAGTCAAGGCCCACTCATTTTGTGTGAGGCTTTCTTTTGTG 720
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QY 721 TGTCTACGCTCCCTCTTCTGTGTGTGTGTGTATGTACAAGTAGCACTAGTGTGTA 780
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QY 841 AACTTACAATCATTTGATTAATCTTGAATCTGAATTTCTAGTTCGGTTGTATGTTAAT 900
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QY 961 AAAGGACGAGATGAGAGATTTTGAATCTGGAAGAGATTAATTCATAGACACTA 1020
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DB 1201 AAAGCTAGGATTTTCAATTTGGGAGTGTACTAGTAATCAATTAATTAACCAAGATGACT 1260
QY 1261 TTCTGATTTTGAATTTTGAAGCTTTTCTTATGTTTAAATAAACAAGTATTAATTAACAAT 1320
DB 1261 TTCTGATTTTGAATTTTGAAGCTTTTCTTATGTTTAAATAAACAAGTATTAATTAACAAT 1320
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DB 1321 AAAAGAAAACATTTTGTGAAAAGAGAAATTAAGTTTACTGACCCCATTTGACAGATG 1380
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DB 1381 TCCCATTAATATCTGATAGAAATGATGAGCAATGAGAAAGTATTTGTCACGGTGACAA 1440
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DB 1441 TCGGAATGTTCTTTTAAAGCTCATCGAACAATCAGAACCGTTGATTTTCCCGCATCA 1500
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QY 1561 ACATTTAGTAATCTCTTGTGAGCGGTGTAACCGGTTAAACGATTTCTTCCCATTTGATC 1620
DB 1561 ACATTTAGTAATCTCTTGTGAGCGGTGTAACCGGTTAAACGATTTCTTCCCATTTGATC 1620
QY 1621 GCTTTTAAACATCTCGTGTGTATCTCCACCGTCCGTTTCTCTCACTAATTTTGA 1677
DB 1621 GCTTTTAAACATCTCGTGTGTATCTCCACCGTCCGTTTCTCTCACTAATTTTGA 1677

RESULT 2
US-09-938-842A-3729
/ Sequence 3729, Application US/0993842A
/ Publication No. US20040009476A9
/ GENERAL INFORMATION:
/ APPLICANT: Harper, Jeff
/ APPLICANT: Kreps, Joel
/ APPLICANT: Wang, Xun
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
/ FILE REFERENCE: SAME, AND METHODS OF USE
/ CURRENT APPLICATION NUMBER: US/09/938,842A
/ PRIOR FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: US 60/227,866
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: US 60/264,647
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/300,111
/ NUMBER OF SEQ ID NOS: 5379
/ SEQ ID NO 3729
/ LENGTH: 1677
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-09-938-842A-3729

Query Match 100.0%; Score 1677; DB 11; Length 1677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      181 TAGGCTTCTATGCTAATGAAATGAGACCGAATGCAATTAACCAAGCATCTTAAGAT 240
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Qy      481 AAGCCTAAAAAGGTACTACCGGTTTGAACCGGTTTAAATTTGTGTTAAATTTCC 540
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Qy      541 GGATCCGTTTGTGTTTAAATCTCAAGGCCAAGTTATCGCAATTTTGAATTTTGAAG 600
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Qy      601 GGTAGGGAATGTTGGGGTCCGAATAGTTGGGCTAGCCCTCAACAATGTGTGAACGTGAAG 660
Db      601 GGTAGGGAATGTTGGGGTCCGAATAGTTGGGCTAGCCCTCAACAATGTGTGAACGTGAAG 660
Qy      661 AAGATGAGGTTCCAGCTCAGGCCCCCAATTCACATTTTGTGTTAGCTTTCTTTCTG 720
Db      661 AAGATGAGGTTCCAGCTCAGGCCCCCAATTCACATTTTGTGTTAGCTTTCTTTCTG 720
Qy      721 TCGTTACGGTCCCTCTTTCTGTGCGGTGCTATGTACAAAGTAAAGTAAAGTAAAGTAAAG 780
Db      721 TCGTTACGGTCCCTCTTTCTGTGCGGTGCTATGTACAAAGTAAAGTAAAGTAAAGTAAAG 780
Qy      781 CCCGAAACAAGTACCAACGAATCAAAATAGTTGAATCGGTTACATCTAGTTACCGTGC 840
Db      781 CCCGAAACAAGTACCAACGAATCAAAATAGTTGAATCGGTTACATCTAGTTACCGTGC 840
Qy      841 AACTTACATCAATTTGATTAATCTTGAATCTGATTTAGTTGCGTTTGAATGTTAAAT 900
Db      841 AACTTACATCAATTTGATTAATCTTGAATCTGATTTAGTTGCGTTTGAATGTTAAAT 900
Qy      901 CCGGATTTGCAAGTACCAAGTAAATGCTATGCTATGATGTGACCGGTTTAAATC 960
Db      901 CCGGATTTGCAAGTACCAAGTAAATGCTATGCTATGATGTGACCGGTTTAAATC 960
Qy      961 AAAGGACGACGATAGAGGATTTTGAATCTCGAAGAAAGATTTATTCATAGACACTA 1020
Db      961 AAAGGACGACGATAGAGGATTTTGAATCTCGAAGAAAGATTTATTCATAGACACTA 1020
Qy      1021 ATTACGTTTGTGTGCGGAGCTTGTGACCTTACATTAATGAGGCTCAACCCCAAGTATG 1080
Db      1021 ATTACGTTTGTGTGCGGAGCTTGTGACCTTACATTAATGAGGCTCAACCCCAAGTATG 1080
Qy      1081 GGCTTACAGCTTTTCCATTAATTAAGTAAATCTTTTGGCTTAAACCAATTAATTAAT 1140
Db      1081 GGCTTACAGCTTTTCCATTAATTAAGTAAATCTTTTGGCTTAAACCAATTAATTAAT 1140
Qy      1141 ATTGAATCTTTCCAAACCATAGAAAAGTTAAATTTGATCAGGATGGAATTTTGTAC 1200

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Db      1141 ATTGAATCTTTCCAAACCATAGAAAAGTTAAATTTGATCAGGATGGAATTTTGTAC 1200
Qy      1201 AAAGCTAGCTATTTCAATTTGGAGTGTACTACTACTAGTACTAACCAGAAATGAGT 1260
Db      1201 AAAGCTAGCTATTTCAATTTGGAGTGTACTACTACTAGTACTAACCAGAAATGAGT 1260
Qy      1261 TTCTGATTTTGGATTTTGAAGCTTTTCTAGGTTTAAAAAACAAGTATTTACTAAACAAT 1320
Db      1261 TTCTGATTTTGGATTTTGAAGCTTTTCTAGGTTTAAAAAACAAGTATTTACTAAACAAT 1320
Qy      1321 AAAAGAAAAACATTTTGTGAAAGAAATTAAGTTTACTGAGACCCCATTTGACAGATGG 1380
Db      1321 AAAAGAAAAACATTTTGTGAAAGAAATTAAGTTTACTGAGACCCCATTTGACAGATGG 1380
Qy      1381 TCCCATTAATTAATGATGATGAGATGAGCAATGGAAGATGTTGTTGACGGGTACAA 1440
Db      1381 TCCCATTAATTAATGATGATGAGATGAGCAATGGAAGATGTTGTTGACGGGTACAA 1440
Qy      1441 TCGGAATGCTTCTTAAAGCTCATCGAACACATCCAGAACCGTTGATTTTCCCGCATCAA 1500
Db      1441 TCGGAATGCTTCTTAAAGCTCATCGAACACATCCAGAACCGTTGATTTTCCCGCATCAA 1500
Qy      1501 AAAGGTTGAATACATATTTCTCACTTGTCTTCTGCTCTATATATATATCTGACGAGTC 1560
Db      1501 AAAGGTTGAATACATATTTCTCACTTGTCTTCTGCTCTATATATATATCTGACGAGTC 1560
Qy      1561 ACATTTAGTAAATCTCTTGGAGAGTGAAGCGGTTTAAACGATCTTTTCCCATTTGATCC 1620
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Qy      1621 GCTTTTAAACAATCTCTGTCATCTCCACCGTCCGTTTCTCTCAGTATATTTTA 1677
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RESULT 3
US-10-087-192-148/c
; Sequence 148, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 174448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174448)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-148

```

```

Query Match      1.4%; Score 23; DB 13; Length 174448;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      223 ACAAGCATCATTAAGATTAAT 245
Db      149367 ACAAGCATCATTAAGATTAAT 149345

```

RESULT 4


```
US-09-930-213-54
; Sequence 54, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHER-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLMINGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SEBS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (4)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-09-930-213-54

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 330;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 148 TTATCCCTCTGTGTGAGACC 168

RESULT 5
US-09-803-719-707
; Sequence 707, Application US/09803719
; Publication No. US20030044783A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Dimaac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kila, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Human Genes and Gene Products
; FILE REFERENCE: 1624.002

US-09-938-842a-3729.olig.rnpb

; CURRENT APPLICATION NUMBER: US/09/803,719
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,609
; NUMBER OF SEQ ID NOS: 2396
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 707
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-719-707

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 394;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 49 TTATCCCTCTGTGTGAGACC 69

RESULT 6
US-10-424-599-103891
; Sequence 103891, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 103891
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64830C.1
US-10-424-599-103891

Query Match
Best Local Similarity 1.3%; Score 21; DB 17; Length 406;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1139 TTATTGAAATCTTCCNACC 1159
DB 254 TTATTGAAATCTTCCNACC 274

RESULT 7
US-09-803-719-1633
; Sequence 1633, Application US/09803719
; Publication No. US20030044783A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
```



```

; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leszkowicz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Human Genes and Gene Products
; FILE REFERENCE: 1624.002
; CURRENT APPLICATION NUMBER: US/09/803,719
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,609
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 2396
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1633
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-938-719-1633

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 407;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 195 TTATCCCTCTGTGTGAGACC 215

RESULT 8
US-09-930-213-306
; Sequence 306, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHÉ-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLMGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 306
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-930-213-306

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 2000;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 885 TTATCCCTCTGTGTGAGACC 905

RESULT 9
US-10-191-807-3/C
; Sequence 3, Application US/10191807
; Publication No. US20030068691A1
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al.
```

```

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001275-PROV
; CURRENT APPLICATION NUMBER: US/10/191,807
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 108359
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(108359)
; OTHER INFORMATION: n = A,T,C or G
; US-10-191-807-3

Query Match
Best Local Similarity 1.3%; Score 21; DB 14; Length 108359;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 TTAATGTTGTGAAGAAATA 260
DB 75869 TTAATGTTGTGAAGAAATA 75849

RESULT 10
US-10-367-094-114/C
; Sequence 114, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 133462
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(133462)
; OTHER INFORMATION: n = A,T,C or G
; US-10-367-094-114

Query Match
Best Local Similarity 1.3%; Score 21; DB 18; Length 133462;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1333 TTTTGAAAGAGAAATAAA 1353
DB 62921 TTTTGAAAGAGAAATAAA 62901

RESULT 11
US-10-027-632-54726/C
; Sequence 54726, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
```



```

; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54726
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-54726
```

```
Query Match          1.2%; Score 20; DB 13; Length 627;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1134 AAAAATTATTTGAAATCTTT 1153
Db      508 AAAAATTATTTGAAATCTTT 489
```

```
RESULT 12
US-10-027-632-294129/c
; Sequence 294129, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294129
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-294129
```

```
Query Match          1.2%; Score 20; DB 13; Length 627;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1134 AAAAATTATTTGAAATCTTT 1153
Db      508 AAAAATTATTTGAAATCTTT 489
```

```
RESULT 13
US-10-027-632-54726/c
; Sequence 54726, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54726
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-54726
```

```
Query Match          1.2%; Score 20; DB 17; Length 627;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1134 AAAAATTATTTGAAATCTTT 1153
Db      508 AAAAATTATTTGAAATCTTT 489
```

```
RESULT 14
US-10-027-632-294129/c
; Sequence 294129, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```


/ PRIOR FILING DATE: 1999-09-28
 / PRIOR APPLICATION NUMBER: US 60/146,002
 / PRIOR FILING DATE: 1999-08-09
 / NUMBER OF SEQ ID NOS: 325720
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 294129
 / LENGTH: 627
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: (1)...(627)
 / OTHER INFORMATION: n = A,T,C or G
 US-10-027-632-294129

Query Match 1.2%; Score 20; DB 17; Length 627;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C 1134 AAAAATTATGAAATCTTT 1153
 DB 508 AAAAATTATGAAATCTTT 489

RESULT 15
 US-10-437-963-9063
 / Sequence 9063, Application US/10437963
 / Publication No. US2004012343A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J.
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / APPLICANT: Wu, Wei
 / APPLICANT: Boukharov, Andrey A.
 / APPLICANT: Barbazuk, Brad
 / APPLICANT: Li, Ping
 / TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 / FILE REFERENCE: 38-21(53221)B
 / CURRENT APPLICATION NUMBER: US/10/437,963
 / CURRENT FILING DATE: 2003-05-14
 / NUMBER OF SEQ ID NOS: 204966
 / SEQ ID NO 9063
 / LENGTH: 628
 / TYPE: DNA
 / ORGANISM: Oryza sativa
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MRT4530_15514C.1
 US-10-437-963-9063

Query Match 1.2%; Score 20; DB 18; Length 628;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1154 CCACCATAGAAAAGTTAAA 1173
 DB 297 CCACCATAGAAAAGTTAAA 316

Search completed: February 28, 2005, 12:54:09
 Job time : 1057.03 secs

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